

Sinedden
10/1007363
Seq. ID 2

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:17:19 ; Search time 36 Seconds
(without alignments)
29.611 Million cell updates/sec

Title: US-10-007-363-2
Perfect score: 48
Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	8	19	AAW54884
2	43	89.6	8	19	AAW54889
3	43	89.6	8	19	AAW54892
4	42	87.5	8	19	AAW54894
5	42	87.5	8	19	AAW54895
6	42	87.5	11	18	AAW17460
7	40	83.3	8	19	AAW54887
8	40	83.3	8	19	AAW54888
9	40	83.3	8	19	AAW54890
10	40	83.3	8	19	AAW54891

11	39	81.2	8	19	AAW54893	Isozyme-specific a
12	38	79.2	8	19	AAW54898	Isozyme-specific a
13	37.5	78.1	14	19	AAW54901	Isozyme-specific a
14	35	72.9	6	19	AAW54886	Isozyme-specific a
15	35	72.9	8	19	AAW54885	Isozyme-specific a
16	35	72.9	14	22	AAW54885	Isozyme-specific a
17	35	72.9	287	21	AAW54941	Protease binding s
18	35	72.9	456	17	AAW54933	Human cancer assoc
19	35	72.9	456	23	AAW54933	Human cancer assoc
20	35	72.9	457	17	AAW54934	Mouse immunophilin
21	35	72.9	649	23	AAW54934	Human immunophilin
22	35	72.9	793	22	AAW54934	Staphylococcus epi
23	35	72.9	1247	22	AAW54934	Novel human diagno
24	34	70.8	10	19	AAW54934	Novel human diagno
25	34	70.8	16	22	AAW54934	E. coli methionyl-
26	34	70.8	16	22	AAW54934	Protease binding s
27	34	70.8	16	22	AAW54934	Protease binding s
28	34	70.8	16	22	AAW54934	Protease binding s
29	34	70.8	17	22	AAW54934	Protease binding s
30	34	70.8	18	22	AAW54934	Protease binding s
31	34	70.8	18	22	AAW54934	Protease binding s
32	34	70.8	18	22	AAW54934	Protease binding s
33	34	70.8	18	22	AAW54934	Protease binding s
34	34	70.8	18	22	AAW54934	Protease binding s
35	34	70.8	18	22	AAW54934	Protease binding s
36	34	70.8	18	22	AAW54934	Protease binding s
37	34	70.8	92	23	AAW54934	Protease binding s
38	34	70.8	122	21	AAW54934	Protease binding s
39	34	70.8	122	23	AAW54934	Protease binding s
40	34	70.8	142	21	AAW54934	Protease binding s
41	34	70.8	205	19	AAW54934	Protease binding s
42	34	70.8	335	22	AAW54934	Protease binding s
43	34	70.8	387	22	AAW54934	Protease binding s
44	34	70.8	458	22	AAW54934	Protease binding s
45	34	70.8	471	22	AAW54934	Protease binding s

ALIGNMENTS

RESULT 1	AAW54884	standard; peptide; 8 AA.
XX	AAW54884	
AC	AAW54884	
XX	AAW54884	
DT	24-SEP-1998	(first entry)
XX		
DE	Isozyme-specific agonist peptide epsilon VI-7:E7.	
XX		
KW	epsilon protein kinase C; ischaemic injury; hypoxic exposure.	
OS	Synthetic.	
PN	W09817299-A1.	
XX		
PD	30-APR-1998.	
XX		
PF	17-OCT-1997; 97WO-US18716.	
XX		
PR	18-OCT-1996; .96US-0028724.	
XX		
PA	(STRD) UNIV LELAND STANFORD JUNIOR.	
XX		
PI	Mochly-Rosen D;	
XX		
DR	WPI, 1998-261181/23.	
XX		
PT	Peptide agonists of protein kinase C - used to reduce ischaemic	
XX		
PS	injury of cells exposed to hypoxic conditions	
XX		
XX	Claim 1; Page 32; 47pp; English.	

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections.

XX Sequence 8 AA;

Query Match 100.0%; Score 48; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPICGD 8
|:|||||
DB 1 HDAPICGD 8

RESULT 2

AAW54889 ID AAW54889 standard; peptide; 8 AA.

XX AC AAW54889;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide epsilon VI-7.5.

XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.

XX Synthetic.

XX WO9817299-A1.

XX 30-APR-1998.

XX PF 17-OCT-1997; 97WO-US18716.

XX PR 18-OCT-1996; 96US-0028724.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 1998-261181/23.

PT Peptide agonists of protein kinase C - used to reduce ischaemic injury of cells exposed to hypoxic conditions

PS Disclosure; Page 32; 47pp; English.

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections.

XX Sequence 8 AA;

Query Match 89.6%; Score 43; DB 19; Length 8;
Best Local Similarity 87.5%; Pred. No. 7.8e+05;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPICGD 8
|:|||||
DB 1 HDAPICGD 8

RESULT 3

AAW54892 ID AAW54892 standard; peptide; 8 AA.

AC AAW54892;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide epsilon VI-7.8.

XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.

XX Synthetic.

XX WO9817299-A1.

XX 30-APR-1998.

XX PF 17-OCT-1997; 97WO-US18716.

XX PR 18-OCT-1996; 96US-0028724.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

XX WPI; 1998-261181/23.

PT Peptide agonists of protein kinase C - used to reduce ischaemic injury of cells exposed to hypoxic conditions

PS Claim 1; Page 32; 47pp; English.

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections.

XX Sequence 8 AA;

Query Match 89.6%; Score 43; DB 19; Length 8;
Best Local Similarity 87.5%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPICGD 8
|:|||||
DB 1 HDAPICGD 8

RESULT 4

AAW54894 ID AAW54894 standard; peptide; 8 AA.

XX AC AAW54894;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide epsilon VI-7.10.

XX epsilon protein kinase C; ischaemic injury; hypoxic exposure.

XX Synthetic.

XX WO9817299-A1.

XX 30-APR-1998.

XX PF 17-OCT-1997; 97WO-US18716.

XX PR 18-OCT-1996; 96US-0028724.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Mochly-Rosen D;

DR WPI: 1998-261181/23.
 XX Peptide agonists of protein kinase C - used to reduce ischaemic
 PT injury of cells exposed to hypoxic conditions
 XX
 PS Claim 1; Page 32; 47pp: English.
 XX
 CC The peptides AAM54879-W54901 are agonists of epsilon protein kinase C
 CC (PKC). They can be used for reducing ischaemic injury to a cell exposed
 CC to hypoxic conditions. They can also be used in a method for
 CC identifying a compound effective to induce preconditioning. The peptides
 CC are administered at a dose of 1-100 microgram administered once to
 CC several times daily in bolus injections.
 XX
 SQ Sequence 8 AA:
 Query Match 87.5%; Score 42; DB 19; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGY 8
 |||||
 DB 1 HDAPLAYD 8

RESULT 5
 AAM54895
 ID AAM54895 standard; peptide; 8 AA.
 XX
 AC AAM54895;
 XX
 DT 24-SEP-1998 (first entry)
 XX
 DE Isozyme-specific agonist peptide epsilon VI-7.11.
 XX
 KW epsilon protein kinase C; ischaemic injury; hypoxic exposure.
 XX
 OS Synthetic.
 XX
 PN MO9817299-A1.
 XX
 PD 30-APR-1998.
 XX
 PF 17-OCT-1997; 97WO-US18716.
 XX
 PR 18-OCT-1996; 96US-0028724.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Mochly-Rosen D;
 XX
 DR WPI: 1998-261181/23.
 XX
 PT Peptide agonists of protein kinase C - used to reduce ischaemic
 PT injury of cells exposed to hypoxic conditions
 XX
 PS Claim 1; Page 32; 47pp: English.
 XX
 CC The peptides AAM54879-W54901 are agonists of epsilon protein kinase C
 CC (PKC). They can be used for reducing ischaemic injury to a cell exposed
 CC to hypoxic conditions. They can also be used in a method for
 CC identifying a compound effective to induce preconditioning. The peptides
 CC are administered at a dose of 1-100 microgram administered once to
 CC several times daily in bolus injections.
 XX
 SQ Sequence 8 AA:
 Query Match 87.5%; Score 42; DB 19; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGY 7
 |||||

DB 1 HDAPIGY 7
 |||||
 DB 5 HDAPIGY 11

RESULT 6
 AAM17460
 ID AAM17460 standard; peptide; 11 AA.
 XX
 AC AAM17460;
 XX
 DT 31-OCT-1997 (first entry)
 XX
 DE Protein kinase C-epsilon peptide delta VI-3 (81-91).
 XX
 KW Signal transduction; cell signalling; modulator; immunomodulator;
 KW protein kinase C; receptor for activated kinase C; RACK;
 KW PKC-epsilon; cognate; graft rejection; autoimmune disease;
 KW allergy; asthma; therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO9714038-A1.
 XX
 PD 17-APR-1997.
 XX
 PF 10-OCT-1996; 96WO-US16195.
 XX
 PR 18-JUN-1996; 96US-0665647.
 PR 10-OCT-1995; 95US-0541964.
 PR 31-JAN-1996; 96US-0594447.
 XX
 PA (TERR) TERRAPIN TECHNOLOGIES INC.
 XX
 PI Kauvar LM, Mochly-Rosen D, Napolitano EW, Ron D;
 PI Vasquez NJ, Voronova A;
 XX
 DR WPI: 1997-236030/21.
 XX
 PT Identifying a modulator of intracellular signal transduction - by
 PT determining the interaction of a signal generating peptide with the
 PT test substance, allows modulation of the immune system
 XX
 PS Claim 9; Page 32; 74pp: English.
 XX
 CC This sequence is a peptide, designated epsilon VI-3, that
 CC corresponds to amino acid residues 81-91 in the VI region of protein
 CC kinase C (PKC)-epsilon. It is can be used as a signal generating
 CC peptide in a claimed method for identifying modulators of
 CC intracellular signal transduction. This method assesses the ability
 CC of candidate modulators to affect the interaction between a signal-
 CC generating protein, such as a PKC isozyme peptide (see AAM15778-79,
 CC AAM15781, AAM15784-85, AAM17452-78), and a cognate binding protein
 CC involved in modulating the signal transduction function. Identified
 CC substances are useful as immunomodulators (claimed). They act to
 CC reduce T-cell activity, reduce the rate of graft rejection, reduce
 CC the severity of an autoimmune disorder, ameliorate allergy and/or
 CC asthma, or diminish a cytokine response (claimed).
 XX
 SQ Sequence 11 AA:
 Query Match 87.5%; Score 42; DB 16; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGY 7
 |||||

DB 5 HDAPIGY 11

RESULT 7
 AAM54887
 ID AAM54887 standard; peptide; 8 AA.
 XX
 AC AAM54887;

XX 24-SEP-1998 (first entry)
 DT Isozyme-specific agonist peptide epsilon VI-7.3.
 DE Epsilon protein kinase C; ischaemic injury; hypoxic exposure.
 XX
 XX Synthetic.
 OS
 XX WO9817299-A1.
 PN 30-APR-1998.
 PD
 XX 17-OCT-1997; 97WO-US18716.
 PF
 XX 18-OCT-1996; 96US-0028724.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PA Mochly-Rosen D;
 PI WPI; 1998-261181/23.
 DR
 XX Peptide agonists of protein kinase C - used to reduce ischaemic
 PT injury of cells exposed to hypoxic conditions
 XX
 PS Claim 1; Page 32; 47pp; English.
 XX
 CC The peptides AAM54879-W54901 are agonists of epsilon protein kinase C
 CC (PKC). They can be used for reducing ischaemic injury to a cell exposed
 CC to hypoxic conditions. They can also be used in a method for
 CC identifying a compound effective to induce preconditioning. The peptides
 CC are administered at a dose of 1-100 microgram administered once to
 CC several times daily in bolus injections.
 XX
 SQ Sequence 8 AA;

Query Match 83.3%; Score 40; DB 19; Length 8;
 Best Local Similarity 87.5%; Pred. No. 7.8e+05;
 Matches 7; Conservative 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 ||| ||||
 Db 1 HDAAGYD 8

RESULT 8
 AAM54888
 ID AAM54888 standard; peptide; 8 AA.
 XX
 AC AAM54888;

XX 24-SEP-1998 (first entry)
 DT Isozyme-specific agonist peptide epsilon VI-7.4.
 DE Epsilon protein kinase C; ischaemic injury; hypoxic exposure.
 XX
 XX Synthetic.
 OS
 XX WO9817299-A1.
 PN 30-APR-1998.
 PD
 XX 17-OCT-1997; 97WO-US18716.
 PF
 XX 18-OCT-1996; 96US-0028724.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PA Mochly-Rosen D;
 PI WPI; 1998-261181/23.

XX Peptide agonists of protein kinase C - used to reduce ischaemic
 PT injury of cells exposed to hypoxic conditions
 XX
 XX Claim 1; Page 32; 47pp; English.
 PS
 CC The peptides AAM54879-W54901 are agonists of epsilon protein kinase C
 CC (PKC). They can be used for reducing ischaemic injury to a cell exposed
 CC to hypoxic conditions. They can also be used in a method for
 CC identifying a compound effective to induce preconditioning. The peptides
 CC are administered at a dose of 1-100 microgram administered once to
 CC several times daily in bolus injections.
 XX
 SQ Sequence 8 AA;

Query Match 83.3%; Score 40; DB 19; Length 8;
 Best Local Similarity 87.5%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 ||| ||||
 Db 1 HDAPIGYD 8

RESULT 9
 AAM54890
 ID AAM54890 standard; peptide; 8 AA.
 XX
 AC AAM54890;

XX 24-SEP-1998 (first entry)
 DT Isozyme-specific agonist peptide epsilon VI-7.6.
 DE Epsilon protein kinase C; ischaemic injury; hypoxic exposure.
 XX
 XX Synthetic.
 OS
 XX WO9817299-A1.
 PN 30-APR-1998.
 PD
 XX 17-OCT-1997; 97WO-US18716.
 PF
 XX 18-OCT-1996; 96US-0028724.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PA Mochly-Rosen D;
 PI WPI; 1998-261181/23.

XX Peptide agonists of protein kinase C - used to reduce ischaemic
 PT injury of cells exposed to hypoxic conditions
 XX
 XX Claim 1; Page 32; 47pp; English.
 PS
 CC The peptides AAM54879-W54901 are agonists of epsilon protein kinase C
 CC (PKC). They can be used for reducing ischaemic injury to a cell exposed
 CC to hypoxic conditions. They can also be used in a method for
 CC identifying a compound effective to induce preconditioning. The peptides
 CC are administered at a dose of 1-100 microgram administered once to
 CC several times daily in bolus injections.
 XX
 SQ Sequence 8 AA;

Query Match 83.3%; Score 40; DB 19; Length 8;
 Best Local Similarity 87.5%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 ||| ||||
 Db 1 HDAAGYD 8

RESULT 10

AAW54891

ID AAW54891 standard; peptide; 8 AA.

AC AAW54891;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide epsilon VI-7.7.

KM epsilon protein kinase C; ischaemic injury; hypoxic exposure.

OS Synthetic.

PN WO9817299-A1.

PD 30-APR-1998.

PF 17-OCT-1997; 97WO-US18716.

PR 18-OCT-1996; 96US-0028724.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Mochly-Rosen D;

DR WPI; 1998-261181/23.

PT Peptide agonists of protein kinase C - used to reduce ischaemic injury of cells exposed to hypoxic conditions

PS Claim 1; Page 32; 47pp; English.

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections.

SQ Sequence 8 AA;

Query Match

83.3%; Score 40; DB 19; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGYD 8

DB 2 DAPIGYD 8

RESULT 11

AAW54893

ID AAW54893 standard; peptide; 8 AA.

AC AAW54893;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide epsilon VI-7.9.

KM epsilon protein kinase C; ischaemic injury; hypoxic exposure.

OS Synthetic.

PN WO9817299-A1.

PD 30-APR-1998.

PF 17-OCT-1997; 97WO-US18716.

PR 18-OCT-1996; 96US-0028724.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Mochly-Rosen D;

DR WPI; 1998-261181/23.

PT Peptide agonists of protein kinase C - used to reduce ischaemic injury of cells exposed to hypoxic conditions

PS Claim 1; Page 32; 47pp; English.

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections.

SQ Sequence 8 AA;

Query Match

81.2%; Score 39; DB 19; Length 8;

Best Local Similarity 87.5%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8

DB 1 HDAPIGYD 8

RESULT 12

AAW54898

ID AAW54898 standard; peptide; 8 AA.

AC AAW54898;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide eta VI-7.

KM epsilon protein kinase C; ischaemic injury; hypoxic exposure.

OS Synthetic.

PN WO9817299-A1.

PD 30-APR-1998.

PF 17-OCT-1997; 97WO-US18716.

PR 18-OCT-1996; 96US-0028724.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Mochly-Rosen D;

DR WPI; 1998-261181/23.

PT Peptide agonists of protein kinase C - used to reduce ischaemic injury of cells exposed to hypoxic conditions

PS Disclosure; Page 32; 47pp; English.

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections.

SQ Sequence 8 AA;

Query Match 79.2%; Score 38; DB 19; Length 8;
 Best Local Similarity 62.5%; Pred. No. 7.8e+05;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 1: 1:1111
 DB 1 HEPPLGYD 8

RESULT 13

AAW54901
 ID AAW54901 standard; peptide; 14 AA.

AC AAW54901;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide epsilon VI-7.1x.

KW epsilon protein kinase C; ischaemic injury; hypoxic exposure.

OS Synthetic.

PN WO9817299-A1.

PD 30-APR-1998.

PF 17-OCT-1997; 97WO-US18716.

PR 18-OCT-1996; 96US-0028724.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Mochly-Rosen D;

DR WPI; 1998-261181/23.

PT Peptide agonists of protein kinase C - used to reduce ischaemic injury of cells exposed to hypoxic conditions

PS Disclosure; Page 32; 47pp; English.

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections.

SQ Sequence 14 AA;

Query Match 78.1%; Score 37.5; DB 19; Length 14;
 Best Local Similarity 88.9%; Pred. No. 1.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 HDAPIGYD 8
 1: 1:111111
 DB 4 HDAPIGDYD 12

RESULT 14

AAW54886
 ID AAW54886 standard; peptide; 6 AA.

AC AAW54886;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide epsilon VI-7.2.

KW epsilon protein kinase C; ischaemic injury; hypoxic exposure.

OS Synthetic.

XX WO9817299-A1.
 PN 30-APR-1998.
 PD 17-OCT-1997; 97WO-US18716.
 PF 18-OCT-1996; 96US-0028724.
 PR (STRD) UNIV LELAND STANFORD JUNIOR.
 PA Mochly-Rosen D;
 DR WPI; 1998-261181/23.
 DT Peptide agonists of protein kinase C - used to reduce ischaemic injury of cells exposed to hypoxic conditions

PS Claim 1; Page 32; 47pp; English.

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed to hypoxic conditions. They can also be used in a method for identifying a compound effective to induce preconditioning. The peptides are administered at a dose of 1-100 microgram administered once to several times daily in bolus injections.

SQ Sequence 6 AA;

Query Match 72.9%; Score 35; DB 19; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIG 6
 1: 1:1111
 DB 1 HDAPIG 6

RESULT 15

AAW54885
 ID AAW54885 standard; peptide; 8 AA.

AC AAW54885;

DT 24-SEP-1998 (first entry)

DE Isozyme-specific agonist peptide epsilon VI-7.1.

KW epsilon protein kinase C; ischaemic injury; hypoxic exposure.

OS Synthetic.

PN WO9817299-A1.

PD 30-APR-1998.

PF 17-OCT-1997; 97WO-US18716.

PR 18-OCT-1996; 96US-0028724.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PI Mochly-Rosen D;

DR WPI; 1998-261181/23.

PT Peptide agonists of protein kinase C - used to reduce ischaemic injury of cells exposed to hypoxic conditions

PS Claim 1; Page 32; 47pp; English.

CC The peptides AAW54879-W54901 are agonists of epsilon protein kinase C (PKC). They can be used for reducing ischaemic injury to a cell exposed

CC to hypoxic conditions. They can also be used in a method for
 CC identifying a compound effective to induce preconditioning. The peptides
 CC are administered at a dose of 1-100 microgram administered once to
 CC several times daily in bolus injections.

XX
 SQ Sequence 8 AA;

Query Match 72.9%; Score 35; DB 19; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIG 6
 111111
 Db 1 HDAPIG 6

Search completed: March 14, 2003, 09:22:00
 Job time : 37 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 14, 2003, 09:21:09 ; Search time 14 Seconds
(without alignments)

16.813 Million cell updates/sec

Title: US-10-007-363-2

Perfect score: 48

Sequence: 1 HDAPRGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCRTUS.COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Backfilest1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	48	100.0	8 4 US-08-953-033-6	Sequence 6, Appl
2	43	89.6	8 4 US-08-953-033-11	Sequence 11, Appl
3	43	89.6	8 4 US-08-953-033-14	Sequence 14, Appl
4	42	87.5	8 4 US-08-953-033-16	Sequence 16, Appl
5	42	87.5	8 4 US-08-953-033-17	Sequence 17, Appl
6	42	87.5	11 1 US-08-594-447-19	Sequence 19, Appl
7	42	87.5	11 1 US-08-541-964-18	Sequence 18, Appl
8	42	87.5	11 2 US-08-665-647-33	Sequence 33, Appl
9	40	83.3	8 4 US-08-953-033-9	Sequence 9, Appl
10	40	83.3	8 4 US-08-953-033-10	Sequence 10, Appl
11	40	83.3	8 4 US-08-953-033-12	Sequence 12, Appl
12	40	83.3	8 4 US-08-953-033-13	Sequence 13, Appl
13	39	81.2	8 4 US-08-953-033-15	Sequence 15, Appl
14	38	79.2	8 4 US-08-953-033-20	Sequence 20, Appl
15	37.5	78.1	14 4 US-08-953-033-23	Sequence 23, Appl
16	35	72.9	6 4 US-08-953-033-8	Sequence 8, Appl
17	35	72.9	8 4 US-08-953-033-7	Sequence 7, Appl
18	35	72.9	649 4 US-09-134-001C-3891	Sequence 3891, Ap
19	34	70.8	10 1 US-08-584-226-22	Sequence 22, Appl
20	34	70.8	500 4 US-09-325-932A-149	Sequence 149, App
21	34	70.8	639 4 US-09-392-772-10	Sequence 10, Appl
22	33	68.8	262 2 US-08-602-359A-35	Sequence 35, Appl
23	32	66.7	11 1 US-08-594-447-26	Sequence 26, Appl
24	32	66.7	11 1 US-08-541-964-25	Sequence 25, Appl
25	32	66.7	11 2 US-08-665-647-40	Sequence 40, Appl
26	32	66.7	102 1 US-07-901-703-5	Sequence 5, Appl
27	32	66.7	102 1 US-08-278-729A-11	Sequence 11, Appl

28	32	66.7	102 1 US-08-155-343A-11	Sequence 11, Appl
29	32	66.7	102 1 US-08-406-672-11	Sequence 11, Appl
30	32	66.7	102 1 US-08-335-583C-50	Sequence 50, Appl
31	32	66.7	102 1 US-08-643-563A-11	Sequence 11, Appl
32	32	66.7	102 1 US-08-643-563A-11	Sequence 11, Appl
33	32	66.7	102 1 US-08-462-623-11	Sequence 11, Appl
34	32	66.7	102 1 US-08-451-953A-11	Sequence 11, Appl
35	32	66.7	102 2 US-08-445-468A-11	Sequence 11, Appl
36	32	66.7	102 2 US-08-461-397A-11	Sequence 11, Appl
37	32	66.7	102 2 US-08-912-084-11	Sequence 11, Appl
38	32	66.7	102 3 US-08-278-730A-11	Sequence 11, Appl
39	32	66.7	102 3 US-08-478-097A-6	Sequence 6, Appl
40	32	66.7	102 3 US-08-445-467-11	Sequence 11, Appl
41	32	66.7	102 3 US-08-480-515A-11	Sequence 11, Appl
42	32	66.7	102 4 US-08-414-033A-11	Sequence 9, Appl
43	32	66.7	102 4 US-08-271-556A-9	Sequence 158, App
44	32	66.7	102 4 US-08-931-854E-158	Sequence 158, App
45	32	66.7	102 4 US-08-981-739-158	Sequence 158, App

ALIGNMENTS:

RESULT 1
US-08-953-033-6
Sequence 6, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOLYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF INVENTIONS: POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ. ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1..8
OTHER INFORMATION: epsilon-PKC residues 85-92; epsilon1v1-7; E7
US-08-953-033-6

Query Match 100.0%; Score 48; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
11111111
DB 1 HDAPIGYD 8

RESULT 2

US-08-953-033-11

Sequence 11, Application US/08953033

Patent No. 6165977

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS

TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM

TITLE OF INVENTION: POSITIONS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 60/028,724

FILE DATE: 18-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Pelthory, Joanne R.

REGISTRATION NUMBER: 42,995

REFERENCE/DOCKET NUMBER: 8600-0174.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880

TELEFAX: 650-324-0960

TELEX:

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Other

LOCATION: 1...8

OTHER INFORMATION: epsilon1-7.5

US-08-953-033-11

Query Match

Best Local Similarity 89.6%; Score 43; DB 4; Length 8;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8

11111111

DB 1 HDAPIGYD 8

US-08-953-033-14

Sequence 14, Application US/08953033

Patent No. 6165977

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS

TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM

TITLE OF INVENTION: POSITIONS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 60/028,724

FILE DATE: 18-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Pelthory, Joanne R.

REGISTRATION NUMBER: 42,995

REFERENCE/DOCKET NUMBER: 8600-0174.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880

TELEFAX: 650-324-0960

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Other

LOCATION: 1...8

OTHER INFORMATION: epsilon1-7.8

US-08-953-033-14

Query Match

Best Local Similarity 89.6%; Score 43; DB 4; Length 8;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8

11111111

DB 1 HDAPIGYD 8

US-08-953-033-16

Sequence 16, Application US/08953033

Patent No. 6165977

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS

TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM

TITLE OF INVENTION: POSITIONS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

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: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/953.033
: FILING DATE: 17-OCT-1997
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/028,724
: FILING DATE: 18-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Pelthory, Joanne R.
: REGISTRATION NUMBER: 42,995
: REFERENCE/DOCKET NUMBER: 8600-0174.30
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-324-0880
: TELEFAX: 650-324-0960
: TELEX:
:
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: No. 6165977e
: LOCATION: 1...8
: OTHER INFORMATION: epsilonV1-7.10
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: US-08-953-033-16
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: Query Match      87.5%; Score 42; DB 4; Length 8;
: Best Local Similarity 87.5%; Pred. No. 1.9e+05;
: Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
:
: QY      1 HDAPIGY 8
:         ||||| 11
:         1 HDAP1AYD 8
:
: Db
:
: RESULT 5
: US-08-953-033-17
: Sequence 17, Application US/08953033
: Patent No. 6165977
:
: GENERAL INFORMATION:
: APPLICANT: Mochly-Rosen, Daria
: TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
: TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
: TITLE OF INVENTION: POSITIONS
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Ave., Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/953.033
: FILING DATE: 17-OCT-1997
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/028,724
: FILING DATE: 18-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Pelthory, Joanne R.
: REGISTRATION NUMBER: 42,995
: REFERENCE/DOCKET NUMBER: 8600-0174.30
:
:
:
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-324-0880
: TELEFAX: 650-324-0960
: TELEX:
:
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: No. 6165977e
: LOCATION: 1...8
: OTHER INFORMATION: epsilonV1-7.11
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: US-08-953-033-17
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: Query Match      87.5%; Score 42; DB 4; Length 8;
: Best Local Similarity 100.0%; Pred. No. 1.9e+05;
: Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
:
: QY      1 HDAPIGY 7
:         ||||| 11
:         1 HDAP1GY 7
:
: Db
:
: RESULT 6
: US-08-594-447-19
: Sequence 19, Application US/08594447
: Patent No. 5776716
:
: GENERAL INFORMATION:
: APPLICANT: Ron, Dorit
: APPLICANT: Napolitano, Eugene W.
: APPLICANT: Voronova, Anna F.
: TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
: TITLE OF INVENTION: BLOCK THE INTERACTION OF FYN WITH PKC-THETA, AND USES
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 75
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888;
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/594,447
: FILING DATE: 31-JAN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22550-20025.24
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 822-0168
: TELEX: 90-4030 MRSNFOERSMWH
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Peptide
: LOCATION: 1...11
: OTHER INFORMATION: /label= epsilon-V1-3

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US-08-594-447-19

Query Match 87.5%; Score 42; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.035;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGY 7
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Db 5 HDAPIGY 11

RESULT 7

US-08-541-964-18

Sequence 18, Application US/08541964

Patent No. 5783405

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: Ron, Dorit

APPLICANT: Kavar, Lawrence M.

APPLICANT: Napolitano, Eugene W.

TITLE OF INVENTION: A RAPID SCREENING METHOD FOR EFFECTORS

TITLE OF INVENTION: OF SIGNAL TRANSDUCTION

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 PENNSYLVANIA AVENUE, NW-STE. 5500

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/541,964

FILING DATE: 10-OCT-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22550-20025.23

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 822-0168

TELEX: 90-4030 MRSNFOERSM

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..11

OTHER INFORMATION: /label= epsilon-VI-3

US-08-541-964-18

Query Match 87.5%; Score 42; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.035;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGY 7
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Db 5 HDAPIGY 11

RESULT 8

US-08-665-647-33

Sequence 33, Application US/08665647

Patent No. 5935803

GENERAL INFORMATION:

APPLICANT: Dasquez, Nicki J.

APPLICANT: Ron, Dorit

APPLICANT: Voronova, Anna F.

APPLICANT: Napolitano, Eugene W.

TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS

TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,647

FILING DATE: 18-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22550-20025.25

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEFAX: (202) 822-0168

TELEX: 90-4030 MRSNFOERSM

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..11

OTHER INFORMATION: /label= epsilon-VI-3

US-08-665-647-33

Query Match 87.5%; Score 42; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.035;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGY 7
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Db 5 HDAPIGY 11

RESULT 9

US-08-953-033-9

Sequence 9, Application US/08953033

Patent No. 6165977

GENERAL INFORMATION:

APPLICANT: Mochly-Rosen, Daria

APPLICANT: ISOZYME-SPECIFIC ACTIVATORS

TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM

TITLE OF INVENTION: POSITIONS

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilon1-7.3
US-08-953-033-9

Query Match 83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
Db 1 HDALIGTD 8

RESULT 10
US-08-953-033-10
Sequence 10, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilon1-7.4
US-08-953-033-10

Query Match 83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 HDAPIGYD 8
Db 1 HDAPIPYD 8

RESULT 11
US-08-953-033-12
Sequence 12, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8

OTHER INFORMATION: epsilonV1-7.6
US-08-953-033-12

Query Match 83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPICVD 8
1 |||||
DB 1 HAAPICVD 8

RESULT 12
US-08-953-033-13

Sequence 13, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
TITLE OF INVENTION: POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pelthoroy, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilonV1-7.7
US-08-953-033-13

Query Match 83.3%; Score 40; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPICVD 8
|||||
DB 2 DAPICVD 8

RESULT 13
US-08-953-033-15

Sequence 15, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
TITLE OF INVENTION: POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pelthoroy, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1...8
OTHER INFORMATION: epsilonV1-7.9
US-08-953-033-15

Query Match 81.2%; Score 39; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPICVD 8
|||||
DB 1 HDAPICVD 8

RESULT 14
US-08-953-033-20

Sequence 20, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
TITLE OF INVENTION: POSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA

US-08-953-033-15

ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petilthory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1..8
OTHER INFORMATION: nvl-7
US-08-953-033-20

Query Match 79.2%; Score 38; DB 4; Length 8;
Best Local Similarity 62.5%; Pred NO. 1.9e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
1: 1:111
Db 1 HETPLGYD 8

RESULT 15
US-08-953-033-23
Sequence 23, Application US/08953033
Patent No. 6165977
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Darla
TITLE OF INVENTION: ISOZYME-SPECIFIC ACTIVATORS
TITLE OF INVENTION: OF PROTEIN KINASE C - METHODS AND COM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/953,033
FILING DATE: 17-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/028,724
FILING DATE: 18-OCT-1996
ATTORNEY/AGENT INFORMATION:

NAME: Petilthory, Joanne R.
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0174.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Other
LOCATION: 1..14
OTHER INFORMATION: epsilon nvl-7.1x
US-08-953-033-23

Query Match 78.1%; Score 37.5; DB 4; Length 14;
Best Local Similarity 88.9%; Pred. NO. 0.33;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 HDAPIG-YD 8
1: 11111111
Db 4 HDAPIGDYD 12

Search completed: March 14, 2003, 09:23:25
Job time: 15 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:21:24 ; Search time 13 seconds

(without alignments)
28.364 Million cell updates/sec

Title: US-10-007-363-2

Perfect score: 48

Sequence: 1 HDAPICVD 8

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues

Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCTI_NEM_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	8	9	US-10-007-363-2
2	48	100.0	156	10	US-09-771-161A-104
3	48	100.0	737	10	US-09-771-161A-195
4	44	91.7	8	9	US-10-007-363-7
5	44	91.7	8	9	US-10-007-363-13
6	42	89.6	8	9	US-10-007-363-8
7	42	87.5	8	9	US-10-007-363-9
8	40	83.3	8	9	US-10-007-363-12
9	40	83.3	8	9	US-10-007-363-14
10	36	75.0	8	9	US-10-007-363-6
11	36	75.0	8	9	US-10-007-363-17
12	35	72.9	8	9	US-10-007-363-10
13	35	72.9	8	9	US-10-007-363-11
14	35	72.9	287	10	US-09-925-301-1386
15	34	70.8	550	10	US-09-841-132-562
16	34	70.8	560	10	US-09-841-132-492
17	34	70.8	677	10	US-09-815-242-10210
18	34	70.8	677	10	US-09-815-242-11921
19	34	70.8	682	10	US-09-815-242-11214

20	34	70.8	704	10	US-09-815-242-13925	Sequence 13925, A
21	34	70.8	1131	10	US-09-801-368-72	Sequence 72, Appl
22	33	68.8	262	9	US-10-027-805-35	Sequence 35, Appl
23	33	68.8	262	10	US-09-903-410-35	Sequence 15, Appl
24	32	66.7	118	12	US-10-115-406-15	Sequence 4, Appl
25	32	66.7	138	10	US-09-925-297-879	Sequence 879, App
26	32	66.7	143	12	US-10-002-278-4	Sequence 11, Appl
27	32	66.7	472	9	US-09-841-758-11	Sequence 1, Appl
28	32	66.7	472	10	US-09-841-758-13	Sequence 3, Appl
29	32	66.7	492	10	US-09-925-300-117	Sequence 1717, Ap
30	32	66.7	575	10	US-09-220-091-7	Sequence 7, Appl
31	32	66.7	648	10	US-09-815-242-10504	Sequence 10504, A
32	32	66.7	896	9	US-09-903-170C-5	Sequence 5, Appl
33	32	66.7	896	10	US-09-903-180B-5	Sequence 5, Appl
34	32	66.7	896	10	US-09-903-171A-5	Sequence 5, Appl
35	32	66.7	896	10	US-09-903-148A-5	Sequence 5, Appl
36	32	66.7	896	10	US-09-903-323A-5	Sequence 5, Appl
37	32	66.7	896	10	US-09-903-323A-5	Sequence 5, Appl
38	32	66.7	896	10	US-09-903-323A-5	Sequence 5, Appl
39	32	66.7	979	10	US-09-903-147A-5	Sequence 5, Appl
40	31	64.6	8	9	US-10-007-363-16	Sequence 16, Appl
41	31	64.6	142	10	US-09-815-242-13015	Sequence 13015, A
42	31	64.6	294	10	US-09-815-242-13076	Sequence 13076, A
43	31	64.6	472	10	US-09-841-758-4	Sequence 4, Appl
44	31	64.6	493	9	US-09-738-626-4893	Sequence 4893, Ap
45	31	64.6	690	10	US-09-815-242-5841	Sequence 5841, Ap

ALIGNMENTS:

RESULT 1
US-10-007-363-2
Sequence 2, Application US/10007363
Patent No. US20020168354A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: Pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209, US00
CURRENT APPLICATION NUMBER: US/10/007,363
CURRENT FILING DATE: 2002-11-09
PRIOR APPLICATION NUMBER: US 60/247,830
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: pseudo-epsilon RACK octapeptide
US-10-007-363-2

Query Match 100.0%; Score 48; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPICVD 8
Db 1 HDAPICVD 8

RESULT 2
US-09-771-161A-104
Sequence 104, Application US/09771161A
Patent No. US20020110811A1
GENERAL INFORMATION:
APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1
CURRENT APPLICATION NUMBER: US/09/771,161A

```

; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 104
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-104

Query Match
Best Local Similarity 100.0%; Score 48; DB 10; Length 156;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPICGD 8
DB 85 HDAPICGD 92

RESULT 3
US-09-771-161A-195
; Sequence 195, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 195
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-195

Query Match
Best Local Similarity 100.0%; Score 48; DB 10; Length 737;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPICGD 8
DB 85 HDAPICGD 92

RESULT 4
US-10-007-363-7
; Sequence 7, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; FILE REFERENCE: 58600-8209 US00
; CURRENT APPLICATION NUMBER: US/10/007,363
; CURRENT FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-7

Query Match
Best Local Similarity 91.7%; Score 44; DB 9; Length 8;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPICGD 8
DB 1 HDAPICGE 8

RESULT 5
US-10-007-363-13
; Sequence 13, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; FILE REFERENCE: 58600-8209 US00
; CURRENT APPLICATION NUMBER: US/10/007,363
; CURRENT FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-13

Query Match
Best Local Similarity 91.7%; Score 44; DB 9; Length 8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPICGD 8
DB 1 HDAPICGD 8

RESULT 6
US-10-007-363-8
; Sequence 8, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; FILE REFERENCE: 58600-8209 US00
; CURRENT APPLICATION NUMBER: US/10/007,363
; CURRENT FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: US 60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-8
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Query Match 89.6%; Score 43; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
DB 1 HDAPVGYE 8

RESULT 7
US-10-007-363-9
; Sequence 9, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; FILE REFERENCE: 58600-8209.US00
; CURRENT FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: US-60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-9

Query Match 87.5%; Score 42; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
DB 1 HDAPVGYE 8

RESULT 8
US-10-007-363-12
; Sequence 12, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; FILE REFERENCE: 58600-8209.US00
; CURRENT FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: US-60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-12

Query Match 83.3%; Score 40; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGYD 8
DB 1 HDAPVGYE 8

DB 2 DAPIGYD 8

RESULT 9
US-10-007-363-14
; Sequence 14, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; FILE REFERENCE: 58600-8209.US00
; CURRENT FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: US-60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-14

Query Match 83.3%; Score 40; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.7e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
DB 1 HDAPVGYE 8

RESULT 10
US-10-007-363-6
; Sequence 6, Application US/10007363
; Patent No. US20020168354A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
; TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
; FILE REFERENCE: 58600-8209.US00
; CURRENT FILING DATE: 2002-11-09
; PRIOR APPLICATION NUMBER: US-60/247,830
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-6

Query Match 75.0%; Score 36; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPIGYD 8
DB 1 HDAPVGYE 8

RESULT 11
US-10-007-363-17
; Sequence 17, Application US/10007363
; Patent No. US20020168354A1

```
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
TITLE OF INVENTION: Ischemia
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/007,363
CURRENT FILING DATE: 2002-11-09
PRIORITY FILING DATE: 2000-11-10
PRIORITY FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-17
```

```
Query Match
Best Local Similarity 75.0%; Score 36; DB 9; Length 8;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 HDAPIGD 8
111111
Db 1 HDGIDGID 8
```

```
RESULT 12
US-10-007-363-10
Sequence 10, Application US/10007363
Patent No. US20020168354A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/007,363
CURRENT FILING DATE: 2002-11-09
PRIORITY FILING DATE: 2000-11-10
PRIORITY FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-10
```

```
Query Match
Best Local Similarity 72.9%; Score 35; DB 9; Length 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HDAPIG 6
111111
Db 1 HDAPIG 6
```

```
RESULT 13
US-10-007-363-11
Sequence 11, Application US/10007363
Patent No. US20020168354A1
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: pseudo-epsilon RACK Peptide Composition
TITLE OF INVENTION: and Method for Protection Against Tissue Damage Due to
FILE REFERENCE: 58600-8209.US00
CURRENT APPLICATION NUMBER: US/10/007,363
```

```
CURRENT FILING DATE: 2002-11-09
PRIORITY APPLICATION NUMBER: US 60/247,830
PRIORITY FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: modified pseudo-epsilon RACK peptide
US-10-007-363-11
```

```
Query Match
Best Local Similarity 72.9%; Score 35; DB 9; Length 8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 HDAPIG 6
111111
Db 1 HDAPIG 6
```

```
RESULT 14
US-09-925-301-1386
Sequence 1386, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIORITY FILING DATE: PCT/US00/05882
PRIORITY FILING DATE: 2000-03-08
PRIORITY APPLICATION NUMBER: 60/124,270
PRIORITY FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1386
LENGTH: 287
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-301-1386
```

```
Query Match
Best Local Similarity 72.9%; Score 35; DB 10; Length 287;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 HDAPIGD 8
111111
Db 16 HDPIPIGID 23
```

```
RESULT 15
US-09-841-132-562
Sequence 562, Application US/09841132
Patent No. US20020061848A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasser A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 562
LENGTH: 550
TYPE: PRT
ORGANISM: C. Trachomatis D serovar
US-09-841-132-562
```

Query Match 70.88; Score 34; DB 10; Length 550;
 Best Local Similarity 100.08; Pred. No. 44;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DAPIGY 7
 |||||
 Db 253 DAPIGY 258

Search completed: March 14, 2003, 09:23:46
 Job time : 14 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:19:59 ; Search time 17 Seconds
(without alignments)
45.240 Million cell updates/sec

Title: US-10-007-363-2

Perfect score: 48

Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	48	100.0	736	1	KIRBCE
2	48	100.0	737	1	S28942
3	48	100.0	737	1	KIRBCE
4	48	100.0	737	1	KIRBCE
5	39	81.2	652	2	T39409
6	39	81.2	659	1	UC4858
7	38	79.2	682	1	A39666
8	38	79.2	683	1	A23690
9	38	79.2	683	1	S29478
10	38	79.2	1025	2	T10259
11	37	77.1	2203	2	T42742
12	35	72.9	180	2	T47414
13	35	72.9	199	2	AC3241
14	35	72.9	371	2	T26389
15	35	72.9	400	2	T41569
16	35	72.9	457	2	UC5422
17	35	72.9	468	2	S45145
18	35	72.9	471	1	S14733
19	35	72.9	471	1	H84363
20	35	72.9	699	2	A38368
21	35	72.9	1023	2	A47296
22	34.5	71.9	553	2	T06499
23	34	70.8	205	2	D71918
24	34	70.8	290	2	S36706
25	34	70.8	304	2	T42554
26	34	70.8	312	2	T50960
27	34	70.8	326	2	T29810
28	34	70.8	326	2	US0169
29	34	70.8	392	2	AB2474

30	34	70.8	411	2	A96985	uncharacterized co
31	34	70.8	423	2	E64157	hypothetical prote
32	34	70.8	432	2	B65190	potassium uptake p
33	34	70.8	483	2	A81226	potassium uptake p
34	34	70.8	483	2	G66072	trk system potassi
35	34	70.8	483	2	AB0458	methionine-trna ii
36	34	70.8	547	2	D84942	methionine-trna ii
37	34	70.8	550	2	H81718	methionine-trna ii
38	34	70.8	550	2	C71567	methionine-trna ii
39	34	70.8	551	2	H81552	methionyl-trna syn
40	34	70.8	551	2	C86506	methionyl-trna syn
41	34	70.8	551	2	H72117	methionine-trna ii
42	34	70.8	658	2	D69431	methionine-trna ii
43	34	70.8	675	2	AF0185	methionine-trna ii
44	34	70.8	677	1	SYECMT	methionine-trna ii
45	34	70.8	677	2	H90993	methionine trna sy

ALIGNMENTS

RESULT 1
KIRBCE
protein kinase C (EC 2.7.1.1) epsilon - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C:Accession: A29880
R:Ohno, S.; Akita, Y.; Konno, Y.; Imajob, S.; Suzuki, K.
Cell 53, 731-741, 1988
A:Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to c
A:Reference number: A29880; MUID:88223367; PMID:3370672
A:Accession: A29880
A:Molecule type: mRNA
A:Residues: 1-736 <OHN>
A:Cross-references: GB:M20014
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thre
A:Note: activity is calcium-independent, phospholipid-dependent, and activated by di
C:Superfamily: protein kinase C delta; protein kinase C zeta-binding repeat homology;
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholip
F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zeta-binding repeat homology <K21>
F:243-292/Domain: protein kinase C zeta-binding repeat homology <K22>
F:405-667/Domain: protein kinase homology <KIN>
F:413-421/Region: protein kinase ATP-binding motif
F:170-201,204,220/Binding site: zinc (His, Cys, Cys) #status predicted
F:103,186,209,212/Binding site: zinc (His, Cys, His, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:256,259,281,284/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:436,455,531,533/Active site: Lys; Glu, Asp, Lys #status predicted
F:702,709/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

Query Match 100.0%; Score 48; EB 1; Length 736;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 85 HDAPIGYD 92

RESULT 2
S28942
protein kinase C (EC 2.7.1.1) epsilon - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
C:Accession: S28942
R:Basta, P.; Strickland, M.B.; Holmes, W.; Loomis, C.R.; Ballas, L.M.; Burns, D.J.
Biochim. Biophys. Acta 1132, 154-160, 1992
A:Title: Sequence and expression of human protein kinase C-epsilon.
A:Reference number: S28942; MUID:93003318; PMID:1382605
A:Accession: S28942
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-737 <BAS>
A:Cross-references: EMBL:X65293; NID:g35494; PIDN:CAA46388.1; PID:g35495
C:Comment: This is a calcium-independent, phospholipid-dependent, serine- and threonine-
of inositol phospholipids. This protein is a receptor for tumor-promoting phorbol ester
C:Genetics:
A:Gene: GDB:PRCCE
A:Cross-references: GDB:128039; OMIM:176975
A:Map position: 3pter-3qter
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; PK
C:Keywords: ATP; duplication; phorbol ester binding; phospholipid binding; phosphotransf
F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
F:406-668/Domain: protein kinase C zinc-binding repeat homology <KIN>
F:414-422/Region: protein kinase ATP-binding motif
F:170-201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPICGD 8
DB 85 HDAPICGD 92

RESULT 3
KIRCE
protein kinase C (EC 2.7.1.-) epsilon - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C:Accession: B26163; B26408; S00216
R:Ono, Y.; Fujii, T.; Ogita, K.; Kikkawa, U.; Igarashi, K.; Nishizuka, Y.
J. Biol. Chem. 263, 6927-6932, 1988
A:Title: The structure, expression, and properties of additional members of the protein
A:Reference number: A92717; MUID:88198270; PMID:2834357
A:Accession: B26163
A:Molecule type: DNA
A:Residues: 1-737 <ONO>
A:Cross-references: GB:M18331; NID:g206182; PIDN:AAA41872.1; PID:g206183
R:Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
A:Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein kind
A:Reference number: A94145; MUID:87147193; PMID:3469647
A:Accession: B26408
A:Molecule type: mRNA
A:Residues: 397-447, 'GGGCGHDDPEPQSGAE', 467, 'LSNPILLIPDQGPILLRQ', 487-545, 'C', 547-636
A:Cross-references: GB:M15523; NID:g206192; PIDN:AAA41877.1; PID:g206193
C:Comment: Protein kinase C epsilon and epsilon' appear to be encoded by the same gene
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; PK
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phosphotransf
F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
F:406-668/Domain: protein kinase ATP-binding motif
F:170-201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPICGD 8
DB 85 HDAPICGD 92

RESULT 4
KINCE
protein kinase C (EC 2.7.1.-) epsilon - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 21-Nov-1997
C:Accession: S02270
R:Schapp, D.; Parker, P.J.; Bristol, A.; Kitz, R.; Knopf, J.
FEBS Lett. 243, 351-357, 1989
A:Title: Unique substrate specificity and regulatory properties of PKC-epsilon:
A:Reference number: S02270; MUID:8913541; PMID:2917656
A:Accession: S02270
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-737 <SCH>
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by dia
C:Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology;
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phosphotransf
F:156-161/Region: pseudophosphorylation motif
F:170-220/Domain: protein kinase C zinc-binding repeat homology <K21>
F:243-292/Domain: protein kinase C zinc-binding repeat homology <K22>
F:406-668/Domain: protein kinase ATP-binding motif
F:170-201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:243,273,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:437,456,532,534/Active site: Lys, Glu, Asp, Lys #status predicted
F:703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPICGD 8
DB 85 HDAPICGD 92

RESULT 5
T39409
hypothetical protein SPBC1361.08c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T39409
R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Badcock, K.; Churcher, C.M.
submitted to the EMBL data library, April 1998
A:Reference number: Z21852
A:Accession: T39409
A:Status: preliminary; translated from GE/EMBL/DDBU
A:Molecule type: DNA
A:Residues: 1-652 <LYN>
A:Cross-references: EMBL:AL022600; PIDN:CAA18661.1; GSPDB:GN00067; SPDB:SPBC1361.08c
A:Experimental source: strain 972h-7; cosmid cl361
C:Genetics:
A:Gene: SPDB:SPBC1361.08c
A:Map position: 2

Query Match 81.2%; Score 39; DB 2; Length 652;
Best Local Similarity 85.7%; Pred. No. 7.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DAPIGYD 8
111111
Db 419 DAPIGYD 425

RESULT 6

JC4858
VLDL receptor precursor - African clawed frog
N:Alternate names: Very low density lipoprotein receptor; vitellogenin receptor
C:Species: Xenopus laevis (African clawed frog)
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Jun-2000
C:Accession: JC4858
R:Okabayashi, K.; Shoji, H.; Nakamura, T.; Hashimoto, O.; Asashima, M.; Sugino, H.
Biochem. Biophys. Res. Commun. 224, 406-413, 1996
A:Title: cDNA cloning and expression of the Xenopus laevis vitellogenin receptor.
A:Reference number: JC4858; MUID:96295501; PMID:8702402
A:Accession: JC4858
A:Molecule type: mRNA
A:Residues: 1-869 <OKA>

A:Cross-references: GB:AB06906; NID:92366772; PIDN:BAA22145.1; PID:92366773
C:Comment: This receptor mediates incorporation of vitellogenin into oocytes.
C:Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology;
C:Keywords: duplication; fatty acid metabolism; glycoprotein; receptor; transmembrane pr
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-869/Product: VLDL receptor #status predicted <MAT>
F:27-793/Domain: extracellular #status predicted <EXT>
F:32-66/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:71-107/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:112-148/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F:153-187/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F:192-228/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F:228-272/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F:277-311/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F:317-354/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F:359-433/Domain: EGF homology <EG1>
F:399-433/Domain: EGF homology <EG2>
F:440-479/Domain: LDL receptor WYTD-containing repeat homology <RW1>
F:480-525/Domain: LDL receptor WYTD-containing repeat homology <RW2>
F:526-568/Domain: LDL receptor WYTD-containing repeat homology <RW3>
F:569-612/Domain: LDL receptor WYTD-containing repeat homology <RW4>
F:613-655/Domain: LDL receptor WYTD-containing repeat homology <RW5>
F:656-698/Domain: LDL receptor WYTD-containing repeat homology <RW6>
F:707-749/Domain: EGF homology <EG3>
F:794-815/Domain: transmembrane #status predicted <TM>
F:816-869/Domain: intracellular #status predicted <CYT>
F:830-834/Region: coated-pit mediated internalization signal
F:150-201,777,786/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:359-370,366-379,381-393,399-409,405-418,420-433,707-720,716-735,737-749/Disulfide bond

Query Match 81.2%; Score 39; DB 1; Length 869;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPICGYD 8
111111
Db 371 HDAPICGYD 378

RESULT 7

A39666
protein kinase C (EC 2.7.1.-) eta - human
N:Alternate names: protein kinase C PKC-L
C:Species: Homo sapiens (man)
C>Date: 08-Nov-1991 #sequence_revision 11-Apr-1997 #text_change 21-Jul-2000
C:Accession: A39666; A42131; S65018
R:Bacher, N.; Zisman, Y.; Berent, E.; Livneh, E.
Mol. Cell. Biol. 11, 126-133, 1991
A:Title: Isolation and characterization of PKC-L, a new member of the protein kinase C-f
A:Reference number: A39666; MUID:91094824; PMID:1986216
A:Accession: A39666
A:Molecule type: mRNA
A:Residues: 1-276, 'YVNECAV', 'SMSSERG', 292-296, 'MRWN', 301, 'PRP', 'GRD', 309-682 <BA2>

A:Cross-references: GB:M55284; NID:9189988; PIDN:AAA60100.1; PID:9189989
A>Note: the cross-reference is to the corrected sequence
R:Bacher, N.; Zisman, Y.; Berent, E.; Livneh, E.
Mol. Cell. Biol. 12, 1404, 1992
A:Title: Isolation and characterization of PKC-L, a new member of the protein kinase
A:Reference number: A42131; MUID:92186874; PMID:1545821
A:Contents: etaLam
A:Accession: A42131
A:Molecule type: mRNA
A:Residues: 277-308 <BA3>

A:Cross-references: GB:M55284
A>Note: this report is a revision to reference A39666
R:Palmer, R.H.; Ridden, J.; Parker, P.J.
FEBS Lett. 356, 5-8, 1994
A:Title: Identification of multiple, novel, protein kinase C-related gene products.
A:Reference number: S51020; MUID:95080426; PMID:7988719
A:Accession: S65018
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 437-470, 'E', 472-538 <PAL>

A:Cross-references: EMBL:S74620; NID:9786485; PIDN:AAB32724.1; PID:9786486
C:Genetics:
A:Gene: GDB:PRKCH; PKC-L; PRKCL
A:Cross-references: GDB:129009
A:Map position: 19q13.4-19q13.4
C:Function:

A:Description: catalyzes protein phosphorylation at Ser or Thr residues
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by di
C:Superfamily: protein kinase C delta; protein kinase C zeta-binding repeat homology
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholip
F:157-162/Region: pseudophosphorylation motif
F:171-221/Domain: protein kinase C zeta-binding repeat homology <K21>
F:245-275,278,294/Binding site: zinc (His, Cys, His, Cys) #status predicted
F:352-613/Domain: protein kinase C zeta-binding repeat homology <K22>
F:360-368/Region: protein kinase ATP-binding motif
F:171-207,205,221/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F:184-187,210,213/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:245-275,278,294/Binding site: zinc (His, Cys, His, Cys) #status predicted
F:258-261,283,286/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F:383,402,478,480/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 79.2%; Score 38; DB 1; Length 682;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPICGYD 8
111111
Db 88 HETPICGYD 95

RESULT 8

A23690
protein kinase (EC 2.7.1.37) eta - mouse
C:Species: Mus musculus (house mouse)
C>Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 16-Jun-2000
C:Accession: A23690
R:Osada, S.; Mizuno, K.; Saito, T.C.; Akita, Y.; Suzuki, K.; Kuroki, T.; Ohno, S.
J. Biol. Chem. 265, 22434-22440, 1990
A:Title: A phorbol ester receptor/protein kinase, nPKC-eta, a new member of the prot
A:Reference number: A23690; MUID:91093089; PMID:2266135
A:Accession: A23690
A:Molecule type: mRNA
A:Residues: 1-683 <OSA>
A:Cross-references: GB:D90242; GB:J05703; NID:9220526; PIDN:BAA14288.1; PID:9220527
C:Function:
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-thre
A>Note: activity is calcium-independent, phospholipid-dependent, and activated by di
C:Superfamily: protein kinase C delta; protein kinase C zeta-binding repeat homology
C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholip
F:158-163/Region: pseudophosphorylation motif
F:172-222/Domain: protein kinase C zeta-binding repeat homology <K21>
F:246-295/Domain: protein kinase C zeta-binding repeat homology <K22>
F:353-614/Domain: protein kinase homology <KIN>

F:361-369/Region: protein kinase ATP-binding motif
 F:172,203,206,222/Binding site: zinc (His, Cys, Cys) #status predicted
 F:165,188,211,214/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:246,276,279,295/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:259,262,284,287/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:384,403,479,481/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 79.2%; Score 38; DB 1; Length 683;
 Best Local Similarity 62.5%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 1:1111
 Db 88 HETPLGYD 95

RESULT 9
 S29478

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999

C:Accession: 160246; S29478
 R:DeKer, L.V.; Parker, P.J.; McIntyre, P.

FEBS Lett. 312, 195-199, 1992

A:Title: Biochemical properties of rat protein kinase C- ϵ expressed in COS cells.
 A:Reference number: 160246; MUID:93050193; PMID:1426252

A:Accession: 160246
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-683 <RES>

A:Cross-references: EMBL:X68400; NID:956915; PIDN:CAA4466.1; PID:956916
 C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
 A:Note: actively is calcium-independent, phospholipid-dependent, and activated by diacyl
 C:Superfamily: protein kinase C delta, protein kinase C zeta-binding repeat homology; pr
 C:Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phospholipid
 F:158-163/Region: pseudophosphorylation motif
 F:172-222/Domain: protein kinase C zinc-binding repeat homology <K21>
 F:246-295/Domain: protein kinase C zinc-binding repeat homology <K22>
 F:363-614/Domain: protein kinase homology <KIN>
 F:361-369/Region: protein kinase ATP-binding motif
 F:172,203,206,222/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:165,188,211,214/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:246,276,279,295/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
 F:259,262,284,287/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
 F:384,403,479,481/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 79.2%; Score 38; DB 1; Length 683;
 Best Local Similarity 62.5%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 1:1111
 Db 88 HETPLGYD 95

RESULT 10
 T10259

RNA-directed DNA polymerase (EC 2.7.7.49) - pteromalid wasp (Nasonia vitripennis) retro
 C:Species: Nasonia vitripennis
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T10259; I44490
 R:Burke, W.D.; Malik, H.S.; Lathe III, W.C.; Eickbush, T.H.

Nature 392, 141-142, 1998

A:Title: Are retrotransposons long-term hitchhikers?
 A:Reference number: 217001; MUID:98175715; PMID:9515960

A:Accession: T10259
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-1025 <BUR>

A:Cross-references: EMBL:L00950; NID:93559783; PIDN:AC34927.1; PID:92317818
 R:Burke, W.D.; Eickbush, D.G.; Xiong, Y.; Jakubczak, J.; Eickbush, T.H.
 Mol. Biol. Evol. 10, 163-165, 1993

A:Title: Sequence relationship of retrotransposable elements R1 and R2 within and bet
 A:Reference number: A44490; MUID:93196484; PMID:8383793

A:Contents: retrotransposable element R2
 A:Accession: I44490

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA
 A:Residues: 314-956, 'O', 'A', '971', 'AA' <BU2>

A:Note: sequence extracted from NCBI backbone (NCBIP:127243)
 C:Genetics:

A:Mobile element: retrotransposon R2
 C:Keywords: nucleotidyltransferase

Query Match 79.2%; Score 38; DB 2; Length 1025;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGY 7
 111111
 Db 709 HETPIGY 715

RESULT 11
 T42742
 voltage-dependent calcium channel alpha 1 chain, isoform CACNA4 - rat

C:Species: Rattus norvegicus (Norway rat)
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C:Accession: T42742
 R:ihara, Y.; Yamada, Y.; Fujii, Y.; Gonor, T.; Yano, H.; Yasuda, K.; Inagaki, N.; Se

MOL. Endocrinol. 9, 121-130, 1995

A:Title: Molecular diversity and functional characterization of voltage-dependent cal
 A:Reference number: 222258; MUID:95280950; PMID:7760845

A:Accession: T42742
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-2203 <IHA>

A:Cross-references: EMBL:D38101; NID:9736711; PIDN:BA07282.1; PID:9736712
 A:Experimental source: Insulinoma RINm5F complementary DNA library

C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
 C:Keywords: calcium channel

Query Match 77.1%; Score 37; DB 2; Length 2203;
 Best Local Similarity 85.7%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGYD 8
 1:111111
 Db 1937 DSPIGYD 1943

RESULT 12
 T47414
 hypothetical protein T28A8.70 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T47414
 R:Punelle, B.; Boutry, M.; Goffeau, A.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.

submitted to the Protein Sequence Database, March 2000

A:Reference number: 224466
 A:Accession: T47414

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-180 <PUR>
 A:Cross-references: EMBL:AL162691

A:Experimental source: cultivar Columbia; BAC clone T28A8
 C:Genetics:

A:Map position: 3
 A:introns: 21/2; 32/2; 91/3; 105/3
 A:Note: T28A8.70

Query Match 72.9%; Score 35; DB 2; Length 180;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIGD 8
 Db 38 HDPIGVD 45

RESULT 13

AC3241
 conserved hypothetical protein Atu6109 [imported] - Agrobacterium tumefaciens (strain C5
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: AC3241
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 ; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AC3241
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-199 <KUR>
 A:Cross-references: GB:AE008690; PIDN:AL46345.1; PID:q17744134; GSPDB:GN00189
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu6109
 A:Genome: plasmid

Query Match 72.9%; Score 35; DB 2; Length 199;
 Best Local Similarity 71.4%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIGYD 8
 Db 127 DGPVGYD 133

RESULT 14

T26389
 hypothetical protein Y105C5B.m - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26389
 R:McMurray, A.
 submitted to the EMBL Data Library, September 1999
 A:Reference number: Z20208
 A:Accession: T26389
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-371 <WIL>
 A:Cross-references: EMBL:AL110479; NID:el542153; PIDN:CAB54361.1; CESP:Y105C5B.m
 A:Experimental source: clone Y105C5B
 C:Genetics:
 A:Gene: CESP:Y105C5B.m
 A:Introns: 24/1; 56/1; 101/3; 138/2; 219/3; 290/3; 332/2

Query Match 72.9%; Score 35; DB 2; Length 371;
 Best Local Similarity 65.7%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIGYD 8
 Db 59 DAPIGYD 65

RESULT 15

T41569
 hypothetical protein SPC736.12c - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T41569
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.

submitted to the EMBL Data Library, May 1998
 A:Reference number: Z21991
 A:Accession: T41569
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-400 <WOO>
 A:Cross-references: EMBL:AL023705; PIDN:CAA19276.1; GSPDB:GN00068; SPDB:SPCC736.12c
 A:Experimental source: strain 972h-; cosmid c736
 C:Genetics:
 A:Gene: SPDB:SPCC736.12c
 A:Map position: 3
 A:Introns: 29/1; 349/1

Query Match 72.9%; Score 35; DB 2; Length 400;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIG 6
 Db 76 HDAPIG 81

Search completed: March 14, 2003, 09:22:26
 Job time : 19 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:16:54 ; Search time 12 Seconds
(without alignments)
27.651 Million cell updates/sec

Title: US-10-007-363-2

Sequence: 1 HDAPIGYD 8

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	736	1 KPCE_RABIT	P10830 oryctolagus
2	48	100.0	737	1 KPCE_HUMAN	Q02156 homo sapien
3	48	100.0	737	1 KPCE_MOUSE	P16054 mus musculu
4	48	100.0	737	1 KPCE_RAT	P09216 ratu
5	38	79.2	682	1 KPCL_HUMAN	P24723 homo sapien
6	38	79.2	683	1 KPCL_MOUSE	P23298 mus musculu
7	38	79.2	683	1 KPCL_RAT	Q64617 ratu
8	38	79.2	1025	1 POZ1_NASVI	Q03278 nasonia vit
9	37	77.1	2203	1 CCAD_RAT	P27732 ratu
10	35	72.9	456	1 FKBS_MOUSE	Q64378 mus musculu
11	35	72.9	457	1 FKBS_HUMAN	Q13451 h 51 kda fk
12	35	72.9	468	1 VATB_HALVO	Q48333 halobacteri
13	35	72.9	471	1 VATB_HALNI	Q09ne4 halobacteri
14	35	72.9	471	1 VATB_HALSA	P25164 halobacteri
15	35	72.9	699	1 CHIT1_BACCI	P20533 bacillus ci
16	35	72.9	1023	1 TSCC_PSEAM	P55019 pseudopleur
17	34	70.8	290	1 UL49_HVEY4	Q00039 equine hebp
18	34	70.8	345	1 CC14_CAEEL	P18834 caenorhandi
19	34	70.8	483	1 TRKH_ECOLI	P21166 escherichia
20	34	70.8	487	1 TRKH_HAELN	P44843 haemophilus
21	34	70.8	547	1 SYM_BUCAL	P57210 buchnera ap
22	34	70.8	550	1 SYM_CHLMU	Q9107 chlamydia m
23	34	70.8	550	1 SYM_CHLUP	Q84033 chlamydia t
24	34	70.8	551	1 SYM_CHLUP	Q92956 chlamydia t
25	34	70.8	658	1 SYM_ARCTU	Q28819 archaeglob
26	34	70.8	676	1 SYM_ECOLI	P00939 escherichia
27	34	70.8	682	1 SYM_HAELN	P3828 haemophilus
28	34	70.8	682	1 SYM_PASMU	P57838 pasteurilla
29	34	70.8	734	1 SYM_BORBU	Q44951 borrelia bu
30	34	70.8	797	1 SYM_ARATH	Q95yn5 arabidopsis
31	34	70.8	804	1 SYM_ORISA	Q92tsi oryza sativ
32	34	70.8	917	1 SYM_CAEEL	Q09070 caenorhandi
33	34	70.8	1131	1 CHS1_YEAST	P08004 saccharomyc

34	33	68.8	156	1	CU55_ARADI	P80518 araneus dta
35	33	68.8	483	1	TRKH_SALTY	Q91612 salmonella
36	33	68.8	554	1	REC_N_VIBCH	P52118 vibrio chol
37	33	68.8	811	1	SYM_TREPA	O83776 treponema p
38	32	66.7	139	1	YS87_MYCTU	Q10810 mycobacteri
39	32	66.7	307	1	UF01_MOUSE	P70362 mus musculu
40	32	66.7	319	1	K6PF_LACDE	P80019 lactobacill
41	32	66.7	324	1	TH14_FUSSH	P23617 fusarium so
42	32	66.7	343	1	UF01_HUMAN	Q92890 homo sapien
43	32	66.7	372	1	DECA_TRICA	Q26874 tritollum c
44	32	66.7	472	1	SBP1_HUMAN	Q13228 homo sapien
45	32	66.7	581	1	AMY1_SCHPO	Q09840 schizosacch

ALIGNMENTS

```

RESULT 1
KPCE_RABIT, STANDARD: PRT: 736 AA.
AC P10830:
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.-) (npkc-epsilon).
GN PKCE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88223367; PubMed=3370672;
RA Ohno S, Akita Y, Kono Y, Imajob S, Suzuki K.;
RT "A novel phorbol ester receptor/protein kinase, npkc, distantly
RL related to the protein kinase C family.";
Cell 53:731-741(1988).
CC -! FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -! FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -! SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC -! SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
-----
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CC EMBL: M20014; AAA31426.1; -
CC PIR: A29880; KIRCE.
CC HSSP: P28667; IPRO.
CC InterPro: IPR000008; C2.
CC InterPro: IPR002219; DAG_pe-bind.
CC InterPro: IPR000719; Euk_pk_kinase.
CC InterPro: IPR000961; pk_kinase_C.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00069; pk_kinase_1.
CC Pfam: PF00130; DAG_pe-bind; 2.
CC Pfam: PF00168; C2; 1.
CC PRINTS: PR00008; DAGPEDOMAIN.
CC PRODOM: PD000001; Euk_pk_kinase_1.
CC SMART: SM00109; C1; 2.
CC SMART: SM00239; C2; 1.
CC SMART: SM00133; S_TK_X; 1.

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DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50004; C2.DOMAIN.2; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS500108; PROTEIN_KINASE_ST; 1.
DR Repeat; ATP-binding; Transferase; Phosphorylation;
KM Serine/threonine-protein kinase; Phospho-ester binding; Zinc.
FT DOMAIN 1
FT 170 220 C2 DOMAIN.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 407 667 PHORBOL-ESTER AND DAG BINDING 2.
FT NP_BIND 413 421 PROTEIN KINASE.
FT BINDING 436 436 ATP (BY SIMILARITY).
FT ACT_SITE 531 531 ATP (BY SIMILARITY).
FT MOD_RES 702 702 BY SIMILARITY.
FT MOD_RES 709 709 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 736 AA; 83515 MW; 261CAFEE59E9BFEBC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 1; Length 736;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 2
KPC_E_HUMAN STANDARD; PRT; 737 AA.
AC 002156; O9UE81.
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN PKCE OR PKCE.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE-93003318; PubMed-1382605;
RA Basta P., Strickland M.B., Holmes W., Loomis C.R., Ballas L.M.,
RA Burns D.J.;
RT "Sequence and expression of human protein kinase C-epsilon.";
RL Biochim. Biophys. Acta 1132:154-160(1992).
RN [2]
RN SEQUENCE OF 1-116 FROM N.A.
RA Waterston R.;
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC -----
CC EMBL; X65293; CAA46388.1;

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DR EMBL; U51244; AAC08855.1;
DR PIR; S28942; S28942.
DR HSSP; P28867; 1PRO.
DR Genew; HGNC:9401; PKCE.
DR MIM; 176975;
DR InterPro; IPR000008; C2.
DR InterPro; IPR002219; DAG-pe-bind.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00130; DAG-pe-bind; 2.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00433; pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRODOM; PD000001; Euk_pkinase; 1.
DR SMART; SM00109; C1; 2.
DR SMART; SM00239; C2; 1.
DR SMART; SM00133; S_TKC; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50004; C2.DOMAIN.2; 1.
DR PROSITE; PS500479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS500108; PROTEIN_KINASE_ST; 1.
DR Repeat; ATP-binding; Transferase; Phosphorylation;
KM Serine/threonine-protein kinase; Phospho-ester binding; Zinc.
FT DOMAIN 1
FT 170 220 C2 DOMAIN.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 408 668 PHORBOL-ESTER AND DAG BINDING 2.
FT NP_BIND 414 422 PROTEIN KINASE.
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT_SITE 532 532 ATP (BY SIMILARITY).
FT MOD_RES 703 703 BY SIMILARITY.
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 737 AA; 83673 MW; 185032D0A091A1F7C64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 1; Length 737;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HDAPIGYD 8
Db 85 HDAPIGYD 92

RESULT 3
KPC_MOUSE STANDARD; PRT; 737 AA.
AC P16054;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
GN PKCE OR PKCE OR PKCEA.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid:10090;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE-69137541; PubMed-2917656;
RA Schaeap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT "Unique substrate specificity and regulatory properties of
RT PKC-epsilon: a rationale for diversity.";
RL FEBS Lett. 243:351-357(1989).
RN [2]
RN SEQUENCE FROM N.A.
RA TISSUE-Brain;
RA MEDLINE-98127436; PubMed-9467942;
RA Wang Q.J., Acs P., Goodnight J., Blumberg P.M., Mischak H.,

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RA Mushinski J.F.:
RT "The catalytic domain of PKC-epsilon, in reciprocal PKC-delta and -
RT epsilon chimeras, is responsible for conferring tumogenicity to
RT NIH3T3 cells, whereas both regulatory and catalytic domains of
RT PKC-epsilon contribute to in vitro transformation.";
RL Oncogene 16:53-60(1998).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA Wheeler D.L.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF028009; AAB84189.1; -.
DR EMBL: AF325507; AAG53692.1; -.
DR PIR: S02270; KIMSCC.
DR HSSP: P28867; IPTC.
DR MGD: MGI:97599; PRKC.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002719; DAG_PE-bind.
DR InterPro: IPR000219; Euk_pkinase.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase_1.
DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK_X; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Repeat: ATP-binding; Transferase; Phosphorylation;
KW Serine/threonine-protein kinase; Phorbol-ester binding; zinc.
FT DOMAIN 1 99 C2 DOMAIN.
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 292 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 408 668 PROTEIN KINASE.
FT NP_BIND 414 422 ATP (BY SIMILARITY).
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT_SITE 532 532 BY SIMILARITY.
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 737 AA; 83560 MW; 7AEBB8CC10C9F57 CRC64;
Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local 100.0%; Pred. No. 0.033;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 HDAPIGYD 8
DB 85 HDAPIGYD 92
RESULT 4
KPEE_RAT ID KPEE_RAT STANDARD: PRT; 737 AA.
AC P09216;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C, epsilon type (EC 2.7.1.-) (nPKC-epsilon).
DE PRKE OR PKCE.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA MEDLINE=88198770; PubMed=2834397;
RX Ono Y.; Fujii T.; Ogita K.; Kikkawa U.; Igarashi K.; Nishizuka Y.;
RT "The structure, expression, and properties of additional members of
RT the protein kinase C family.";
RL J. Biol. Chem. 263:6927-6932(1988).
RN [2]
RP SEQUENCE OF 135-297 FROM N.A.
RX MEDLINE=88083621; PubMed=3691811;
RA Ono Y.; Fujii T.; Ogita K.; Kikkawa U.; Igarashi K.; Nishizuka Y.;
RT "Identification of three additional members of rat protein kinase C
RT family: delta-, epsilon- and zeta-subspecies.";
RL FEBS Lett. 226:125-128(1987).
CC -!- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M18331; AAA41872.1; -.
DR PIR: B28163; KIRKCC.
DR HSSP: P28867; IPTC.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase_1.
DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK_X; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.

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DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Repeat: ATP-binding; Transferase; Phosphorylation;
  Serine/threonine-protein kinase; Phosphol-ester binding; Zinc.
FT DOMAIN 1 99 C2 DOMAIN
FT DOMAIN 170 220 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 243 222 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 408 668 PROTEIN KINASE.
FT NP_BIND 414 422 ATP (BY SIMILARITY).
FT BINDING 437 437 ATP (BY SIMILARITY).
FT ACT_SITE 532 532 BY SIMILARITY.
FT MOD_RES 703 703 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT MOD_RES 710 710 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 737 AA; 83478 MW; 6AD8999EFD2659F CRC64;

Query Match 100.0%; Score 48; DB 1; Length 737;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HDAPICVD 8
Db 85 HDAPICVD 92

RESULT 5
KPC_L_HUMAN STANDARD; PRT; 682 AA.
ID KPC_L_HUMAN STANDARD; PRT; 682 AA.
AC P24723; Q16246;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein kinase C, eta type (EC 2.7.1.-) (PKC-eta) (PKC-L).
PR KCH OR PKCL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=91094824; PubMed=1986216;
RA Bacher N., Zisman Y., Berent E., Livneh E.;
RT "Isolation and characterization of PKC-L, a new member of the protein
  kinase C-related gene family specifically expressed in lung, skin,
  and heart."
RT Mol. Cell. Biol. 11:126-133(1991).
RN (2)
RP REVISIONS.
RX MEDLINE=92186874; PubMed=1545821;
RA Bacher N., Zisman Y., Berent E., Livneh E.;
RN Mol. Cell. Biol. 12:1404-1404(1992).
RN (3)
RX SEQUENCE OF 437-538 FROM N.A.
RX MEDLINE=95080426; PubMed=7988719;
RA Palmer R.H., Ridden J., Parker P.J.;
RT "Identification of multiple, novel, protein kinase C-related gene
  products."
RT FEBS Lett. 356:5-8(1994).
CC -1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
  SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
  PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
  THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LUNG TISSUE, LESS IN HEART
  AND SKIN TISSUE.
CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
  BINDING DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M55284; AAA60100.1; -
DR EMBL: S74620; AAB32724.1; -
DR PIR: A39666; A39666.
DR HSSP: P28867; IPTO.
DR Genew: HGNC:9403; PKCH.
DR MIM: 605437; -
DR InterPro: IPR000008; C2.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00433; Pkinase_C; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR Prodom: PD000001; Euk_Pkinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR PROSITE: PS00004; C2 DOMAIN 2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS00081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Repeat: ATP-binding; Transferase;
  Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT DOMAIN 12 112 C2 DOMAIN
FT DOMAIN 171 221 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 245 294 PHORBOL-ESTER AND DAG BINDING 2.
FT DOMAIN 354 613 PROTEIN KINASE.
FT NP_BIND 360 368 ATP (BY SIMILARITY).
FT BINDING 383 383 ATP (BY SIMILARITY).
FT ACT_SITE 478 478 BY SIMILARITY.
FT CONFLICT 471 471 D->E (IN REF. 3).
SQ SEQUENCE 682 AA; 77563 MW; 13D4EB01F35AB8 CRC64;

Query Match 79.2%; Score 38; DB 1; Length 682;
Best Local Similarity 62.5%; Pred. No. 3.9;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAPICVD 8
Db 88 HETPLGVD 95

RESULT 6
KPC_L_MOUSE STANDARD; PRT; 683 AA.
ID KPC_L_MOUSE STANDARD; PRT; 683 AA.
AC P23298;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein kinase C, eta type (EC 2.7.1.-) (nPKC-eta) (PKC-L).
GN PKCH OR PKCH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RP TISSUE=Epidermis;
RX MEDLINE=91093089; PubMed=2266135;
RA Osada S.I., Mizuno K., Saito T.C., Akita Y., Suzuki K., Kuroki T.,

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AC 064617:
DT 01-NOV-1997 (Rel. 35 Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein kinase C, eta type (EC 2.7.1.-) (PKC-eta) (PKC-L).
DE PRKH OR PKCH.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lung;
RX MEDLINE=93050193; PubMed=142652;
RA Dexter L.V., Parker P.J., McIntyre P.;
RT "Biochemical properties of rat protein kinase C-eta expressed in COS
RT cells";
RT FEBS Lett. 312:195-199(1992).
CC -1- FUNCTION: THIS IS CALCIUM-INDEPENDENT, PHOSPHOLIPID-DEPENDENT,
CC SERINE- AND THREONINE-SPECIFIC ENZYME.
CC -1- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC -1- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PKC SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X68400; CAA8466.1; -
DR HSSP: P28867; IPRQ.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000961; Pkinase.C.
DR InterPro: IPR002260; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00130; DAG_PE-bind; 2.
DR Pfam: PF00168; C2; 1.
DR Pfam: PF00433; pkinase.C; 1.
DR PRINTS: PR00008; DAGPEDOMAIN.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00109; C1; 2.
DR SMART: SM00239; C2; 1.
DR SMART: SM00133; S_TR_X; 1.
DR SMART: SM00220; S_TRK; 1.
DR PROSITE: PS50004; C2_DOMAIN_2; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 2.
DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 2.
DR PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Transferase; Serine/threonine-protein kinase;
KW Phorbol-ester binding; Zinc; Repeat.
FT DOMAIN 12 102 C2 DOMAIN.
FT DOMAIN 172 222 PHORBOL-ESTER AND DAG BINDING 1.
FT DOMAIN 246 295 PHORBOL-ESTER AND DAG BINDING 2.
FT NP_BIND 355 614 PROTEIN KINASE.
FT BINDING 361 369 ATP (BY SIMILARITY).
FT BINDING 384 384 ATP (BY SIMILARITY).
FT ACT_SITE 479 479 BY SIMILARITY.
SQ SEQUENCE 683 AA; 77946 MW; 2F5B7078D1206510 CRC64;

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Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HDAP1GYD 8
1:1111
Db 88 HEP16GYD 95

RESULT 8

PO21_NASVI

ID PO21_NASVI STANDARD; PRT: 1025 AA.

AC 003278;

DT 01-JUN-1994 (Rel. 29, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Retrovirus-related POL polypeptide from type I retrotransposable

DE element R2 (contains: Reverse transcriptase (EC 2.7.7.49);

DE Endonuclease (Fragment).

OS *Nasona vitripennis* (Parasitic wasp).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;

OC Chalcidoidea; Pteromalidae; *Nasonia*.

OX NCBI_TaxID=7425;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93196484; PubMed=8383793;

RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;

RT "Sequence relationship of retrotransposable elements R1 and R2 within

RT and between divergent insect species.";

RL Mol. Biol. Evol. 10:163-185(1993).

RN [2]

RP REVISIONS.

RA Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate

CC + [DNA](N).

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 CC or send an email to license@sib-sib.ch).

CC EMBL: L00950; AAC34927.1; -

CC PIR: I44490; I44490.

CC InterPro: IPR000477; RYTse.

CC InterPro: IPR000822; Znf_C2H2.

CC Pfam: PF00078; Znf_C2H2.

CC Pfam: PF00096; Zf_C2H2; 1.

CC SMART: SM00355; Znf_C2H2; 1.

CC PROSITE: PS00028; ZINC_FINGER_C2H2_1; 1.

CC PROSITE: PS0157; ZINC_FINGER_C2H2_2; 1.

KM Transposase; RNA-directed DNA polymerase; Transposable element;

KM Hydroxylase; Nuclease; Endonuclease; Zinc-finger.

FT NON_TER

FT DOMAIN

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

AC P27732; Q63491; Q63492; Q62691; Q01542; Q09022; Q09023; Q09024;

AC Q62815;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium

DE channel, L type, alpha-1 polypeptide, isoform 2) (Rat brain class D)

DE (RBD).

DE CACNA1D OR CACNA1A2 OR CCHLA2 OR CAC3 OR CACNA.

OS *Rattus norvegicus* (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Rattus*.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS CACNA4 AND CACNA4B).

RX MEDLINE=95280950; PubMed=7760845;

RA Ihara Y., Yamada Y., Fujii Y., Gonoi T., Yano H., Yasuda K.,

RA Inagaki N., Seino Y., Seino S.;

RT "Molecular diversity and functional characterization of voltage-

RT dependent calcium channels (CACNA4) expressed in pancreatic beta-

RT cells.";

RL Mol. Endocrinol. 9:121-130(1995).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS TRUNCATED; RB9; RB11; RB34 AND RB48).

RX MEDLINE=91299338; PubMed=1648940;

RA Hui A., Ellinor P.T., Krizanov O., Wang J.-J., Diebold R.J.,

RA Schwartz A.;

RT "Molecular cloning of multiple subtypes of a novel rat brain isoform

RT of the alpha-1 subunit of the voltage-dependent calcium channel.";

RL Neuron 7:35-44(1991).

RN [3]

RP SEQUENCE OF 1-125 FROM N.A.

RX MEDLINE=96040125; PubMed=7553731;

RA Kamp T.J., Mitas M., Fields K.L., Asch S., Chin H., Marban E.,

RA Nirenberg M.;

RT "Transcriptional regulation of the neuronal L-type calcium channel

RT alpha 1D subunit gene.";

RL Cell. Mol. Neurobiol. 15:307-326(1995).

RN [4]

RP SEQUENCE OF 1100-1410 FROM N.A. (ISOFORMS RKCS AND RKCS6).

RX MEDLINE=93066265; PubMed=1279681;

RA Yu A.S.-L., Hebert S.C., Brenner B.M., Lytton J.;

RT "Molecular characterization and nephron distribution of a family of

RT transcripts encoding the pore-forming subunit of Ca2+ channels in the

RT kidney.";

RL Proc. Natl. Acad. Sci. U.S.A. 89:10494-10498(1992).

RN [5]

RP SEQUENCE OF 1218-1498 FROM N.A. (ISOFORM ROB3).

RX MEDLINE=96074617; PubMed=7479909;

RA Barry E.L.R., Gesek F.A., Froehner S.C., Friedman P.A.;

RT "Multiple calcium channel transcripts in rat osteosarcoma cells:

RT selective activation of alpha 1D isoform by parathyroid hormone.";

RL Proc. Natl. Acad. Sci. U.S.A. 92:10914-10918(1995).

RN [6]

RP SEQUENCE OF 1200-1493 FROM N.A. (ISOFORMS RH1; RH2; CACH3A/B AND

RX MEDLINE=97376179; PubMed=9232351;

RA Breton H.M., Harland M.L., Frosch M., Petronijevic T.,

RA Barritt G.J.;

RT "Novel variants of voltage-operated calcium channel alpha-1 subunit

RT transcripts in a rat liver-derived cell line: deletion in the IVS4

RT voltage sensing region.";

RL Cell Calcium 22:39-52(1997).

RN [7]

RP SEQUENCE OF 1307-1479 FROM N.A. (ISOFORM RH-55).

RX MEDLINE=90239020; PubMed=1692134;

RA Snutch T.P., Leonard J.P., Gilbert M.M., Luster H.A., Davidson N.;

RT "Rat brain expresses a heterogeneous family of calcium channels.";

Proc. Natl. Acad. Sci. U.S.A. 87:3391-3395(1990).

-1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDATE THE ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION, CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-1D GIVES RISE TO L-TYPE CALCIUM CURRENTS. LONG-LASTING (L-TYPE) CALCIUM CHANNELS BELONG TO THE "HIGH-VOLTAGE ACTIVATED" (HVA) GROUP. THEY ARE BLOCKED BY DIHYDROPYRIDINES (DHP).

CC PHENYALKYLAMINES, BENZOTHAZEPINES, AND BY OMEGA-AGATOXIN-111A (OMEGA-ACA-111A). THEY ARE HOWEVER INSENSITIVE TO OMEGA-CONOTOXIN-GVIA (OMEGA-CTX-GVIA) AND OMEGA-AGATOXIN-11A (OMEGA-AGA-11A).

CC -1- SUBUNIT: VOLTAGE-DEPENDENT CALCIUM CHANNELS ARE MULTISUBUNIT COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITS IN A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORE-FORMING AND VOLTAGE-SENSITIVE ALPHA-1 SUBUNIT. IN MANY CASES, THIS SUBUNIT IS SUFFICIENT TO GENERATE VOLTAGE-SENSITIVE CALCIUM CHANNEL ACTIVITY. THE AUXILIARY SUBUNIT BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC CACNA4/RB48/RBD-55, Delta-IV-S3, Delta-IV-S4, RB9, RB11, RB34 RB1, RH2, RKC5, RKC6, ROB3 and a truncated isoform, are produced by alternative splicing. The region sequenced in isoforms ROB3 and RKC5 is identical to CACNA4.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, PANCREATIC ISLETS AND B-LYMPHOCYTES.

CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS FAMILY.

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CC -----

DR EMBL: D38101; BAA07282.1; -

DR EMBL: D38102; BAA07283.1; -

DR EMBL: M57682; AAA42015.1; -

DR EMBL: U14005; AAB60515.1; -

DR EMBL: M99221; AAA40895.1; -

DR EMBL: U31772; AAA89156.1; -

DR EMBL: U49126; AAB61634.1; -

DR EMBL: U49127; AAB61635.1; -

DR EMBL: U49128; AAB61636.1; -

DR InterPro: IPR001682; Ca/Na_pore.

DR InterPro: IPR002077; Ca_channel.

DR InterPro: IPR003091; K_channel.

DR InterPro: IPR000636; M_channel_nlg.

DR Pfam: PF00520; Ion_trans_4.

DR PRINTS: PR00167; CACHANNEL.

DR PRINTS: PR00169; KCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family;

KW Calcium-binding; Phosphorylation; Alternative splicing.

FT REPEAT 112 408 I.

FT REPEAT 528 774 II.

FT REPEAT 892 1174 III.

FT REPEAT 1211 1486 IV.

FT DOMAIN 1 126 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 127 145 S1 OF REPEAT I (POTENTIAL).

FT DOMAIN 146 163 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 164 183 S2 OF REPEAT I (POTENTIAL).

FT DOMAIN 184 195 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 196 214 S3 OF REPEAT I (POTENTIAL).

FT	DOMAIN	215	235	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	236	254	S4 OF REPEAT I (POTENTIAL).
FT	DOMAIN	255	273	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	274	293	S5 OF REPEAT I (POTENTIAL).
FT	DOMAIN	294	381	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	382	406	S6 OF REPEAT I (POTENTIAL).
FT	DOMAIN	407	582	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	583	602	S1 OF REPEAT II (POTENTIAL).
FT	DOMAIN	603	617	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	618	636	S2 OF REPEAT II (POTENTIAL).
FT	DOMAIN	637	644	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	645	663	S3 OF REPEAT II (POTENTIAL).
FT	DOMAIN	664	673	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	674	692	S4 OF REPEAT II (POTENTIAL).
FT	DOMAIN	693	711	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	712	732	S5 OF REPEAT II (POTENTIAL).
FT	DOMAIN	733	786	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	787	811	S6 OF REPEAT II (POTENTIAL).
FT	DOMAIN	812	945	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	946	964	S1 OF REPEAT III (POTENTIAL).
FT	DOMAIN	965	980	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	981	1000	S2 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1001	1012	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1013	1031	S3 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1032	1037	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1038	1057	S4 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1058	1076	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1077	1096	S5 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1097	1186	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1187	1207	S6 OF REPEAT III (POTENTIAL).
FT	DOMAIN	1208	1264	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1265	1283	S1 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1284	1298	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1299	1318	S2 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1319	1325	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1326	1347	S3 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1348	1357	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1358	1377	S4 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1378	1396	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1397	1416	S5 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1417	1483	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1484	1508	S6 OF REPEAT IV (POTENTIAL).
FT	DOMAIN	1509	2203	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	2204	2203	POLY-MET.
FT	DOMAIN	2204	2203	POLY-LEU.
FT	TRANSMEM	2204	2203	POLY-GLU.
FT	DOMAIN	2204	2203	BINDING TO THE BETA SUBUNIT (BY SIMILARITY).
FT	TRANSMEM	2204	2203	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
FT	DOMAIN	2204	2203	CALCIUM ION SELECTIVITY AND PERMEABILITY (BY SIMILARITY).
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FT				

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96074651; PubMed=7479941;
 RA Yen W.-C., Li T.-K., Blierer B.E., McKnight S.L.;
 RT "Identification and characterization of an immunophilin expressed
 during the clonal expansion phase of adipocyte differentiation.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11081-11085(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Thymus;
 RX MEDLINE=95349606; PubMed=7542743;
 RA Baughman G., Wiederech G.J., Campbell N.F., Martin M.M.,
 RA Bourgeois S.;
 RT "FKBP5, a novel T-cell-specific immunophilin capable of calcineurin
 inhibition.";
 RL Mol. Cell. Biol. 15:4395-4402(1995).
 CC -1- FUNCTION: INTERACTS WITH PROGESTERONE RECEPTOR (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- ENZYME REGULATION: INHIBITED BY BOTH FK506 AND RAPAMYCIN.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, HIGHEST LEVELS FOUND IN THE
 LIVER, SKELETAL MUSCLE, KIDNEY AND THYMUS. EXPRESSION IS REGULATED
 DURING ADIPOCYTE DIFFERENTIATION.
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PI3ASE FAMILY. CONTAINS 2
 FKBP-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 TPR REPEATS.
 CC -----
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 CC -----
 DR EMBL: U36220; AAA89162.1; -;
 DR EMBL: U16959; AAA86983.1; -;
 DR HSSP: P27124; 1ROT.
 DR MGD: MGI:104670; Fkbp5.
 DR InterPro: IPR001179; FKBP_PPIase.
 DR InterPro: IPR001440; TPR.
 DR Pfam: PF00254; FKBP; 2.
 DR Pfam: PF00515; TPR; 2.
 DR PROSITE: PS00453; FKBP_PPIASE_1; 1.
 DR PROSITE: PS00454; FKBP_PPIASE_2; 1.
 DR PROSITE: PS00509; FKBP_PPIASE_3; 2.
 KW isomerase; Rotamase; TPR repeat; Repeat; Nuclear protein.
 FT DOMAIN 50 138 PPIASE, FKBP-TYPE 1.
 FT REPEAT 165 251 TPR 1.
 FT REPEAT 268 301 TPR 2.
 FT REPEAT 317 350 TPR 3.
 FT REPEAT 352 384 TPR 3.
 SQ SEQUENCE 456 AA; 50966 MW; 8FDD0C9B61478EB46 CRC64;
 Query Match 72.9%; Score 35; DB 1; Length 456;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 51 kDa FK506-binding protein (FKBP51) (peptidyl-prolyl cis-trans
 DE isomerase) (EC 5.2.1.8) (PPIase) (Rotamase) (54 kDa progesterone
 DE receptor-associated immunophilin) (FKBP54) (P54) (PFI antigen)
 DE (HSP90-binding immunophilin) (Androgen-regulated protein 6).
 GN FKBP5 OR AIG6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thymus;
 RX MEDLINE=97242207; PubMed=9125197;
 RA Baughman G., Wiederech G.J., Chang F., Martin M.M., Bourgeois S.;
 RT "Tissue distribution and abundance of human FKBP51, an FK506-binding
 protein that can mediate calcineurin inhibition.";
 RL Biochem. Biophys. Res. Commun. 232:437-443(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhang J.S., Smith D.I.;
 RT "Identification of AIG6 as an androgen response gene in human prostate
 cancer cell line LNCaP.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 9-457 FROM N.A.
 RX MEDLINE=97154494; PubMed=9001212;
 RA Nair S.C., Riherman R.A., Toran E.J., Chen S., Prapapanich V.,
 RA Butts R.N., Smith D.F.;
 RT "Molecular cloning of human FKBP51 and comparisons of immunophilin
 interactions with Hsp90 and progesterone receptor.";
 RL Mol. Cell. Biol. 17:594-603(1997).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=94043261; PubMed=7693698;
 RA Smith D.F., Alberts M.W., Schreiber S.L., Leach K.L., Deibel M.R. Jr.;
 RT "FKBP5, a novel FK506-binding protein in avian progesterone receptor
 complexes and HeLa extracts.";
 RL J. Biol. Chem. 268:24270-24273(1993).
 CC -1- FUNCTION: INTERACTS WITH FUNCTIONALLY MATURE HETERO-OLIGOMERIC
 PROGESTERONE RECEPTOR COMPLEXES ALONG WITH HSP90 AND P23.
 CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
 PEPTIDE BONDS IN OLIGOPEPTIDES.
 CC -1- ENZYME REGULATION: INHIBITED BY FK506 NOT NOT CYCLOSPORIN.
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, ENRICHED IN TESTIS COMPARED
 TO OTHER TISSUES.
 CC -1- INDUCTION: By androgen.
 CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PI3ASE FAMILY. CONTAINS 2
 FKBP-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 TPR REPEATS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U71321; AAC51189.1; -;
 DR EMBL: AF194172; AAL54872.1; -;
 DR EMBL: U42031; AAA86245.1; -;
 DR HSSP: P27124; 1ROT.
 DR GeneW: HGNC:3721; FKBP5.
 DR MIM: 602623; -;
 DR InterPro: IPR001179; FKBP_PPIase.
 DR InterPro: IPR001440; TPR.
 DR Pfam: PF00254; FKBP; 2.
 DR Pfam: PF00515; TPR; 2.
 DR PROSITE: PS00453; FKBP_PPIASE_1; 1.
 DR PROSITE: PS00454; FKBP_PPIASE_2; 1.

DR PROSITE; PSS0059; FKBP_PPIASE_3; 2.
 KW Isomerase; Rotamase; TPR repeat; Repeat; Nuclear protein.
 FT DOMAIN 42 130 PPIASE, FKBP-TYPE 1.
 FT DOMAIN 157 243 PPIASE, FKBP-TYPE 2.
 FT REPEAT 268 301 TPR 1.
 FT REPEAT 317 350 TPR 2.
 FT REPEAT 352 384 TPR 3.
 SO SEQUENCE 457 AA; 51212 MW; 18A86608C6891A73 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 457;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 DB 196 HDIPIGID 203

RESULT 12
 ID VATE_HALVO STANDARD; PRT; 468 AA.

AC 048333;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit B).

GN Halobacterium volcanii (Haloflex volcanii).
 OS Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Haloflex.
 OX NCBI_TaxID=2246;

RP SEQUENCE FROM N.A. AND CHARACTERIZATION.

RC SPRAIN-WR 340;
 RX MEDLINE-95322432; PubMed-7599166.

RA Steinert K., Kirsch-Panic P.G., Bickel-Sandkoeetter S.;

RT "Nucleotide sequence of the ATPase A- and B-subunits of the halophilic archaebacterium Haloflex volcanii and characterization of the enzyme."

RL Blochm. Biophys. Acta 1249:137-144(1995).

CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE ARCHAEL BETA CHAIN IS A REGULATORY SUBUNIT.

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate + H(+) (out).

CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.

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CC EMBL: X79516; CA56052.1;
 DR InterPro: IPR000793; ATPase_a/bC.
 DR InterPro: IPR004100; ATPase_a/bN.
 DR InterPro: IPR00194; ATPase_a/bcentre.
 DR Pfam: PF00006; ATP-synt_ab.1.
 DR Pfam: PF00306; ATP-synt_ab.C.1.
 DR Pfam: PF02874; ATP-synt_ab.N.1.
 DR TIGRFAMs: TIGR01041; ATP_syn_B_arch.1.
 DR PROSITE: PS00152; ATPASE_ALPHA_BETA; 1.
 DR Hydrolyase; ATP synthetase; Hydrogen ion transport.
 KW SEQUENCE 468 AA; 52018 MW; B97D059AEF6071BB CRC64;

Query Match 72.9%; Score 35; DB 1; Length 468;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIGYD 8

DB 20 DEPIGYD 26

RESULT 13
 ID VATE_HALNI STANDARD; PRT; 471 AA.

AC 09HNE4;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit B).

GN ATPB OR VNG2138G.

OS Halobacterium sp. (strain NRC-1).

OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;

OC Halobacteriaceae; Halobacterium.

OX NCBI_TaxID=64091;

RP SEQUENCE FROM N.A.

RX MEDLINE-20504483; PubMed-11016950;

RA Ng W.V., Kennedy S.P., Mahaffas G.G., Bergquist B., Pan M.,

RA Shukla H.D., Lasky S.R., Ballya N.S., Thorsson V., Shroona J.,

RA Swartzell S., Weir D., Hall J., Dahl T.A., Walt R., Goo Y.A.,

RA Lettner B., Keller K., Cruz R., Danos M.J., Hough D.W.,

RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angewine C.M., Dale H.,

RA Isenbarger T.A., Peck R.F., Pohlshöder M., Spudich J.L., Jung K.-H.,

RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;

RT "Genome sequence of Halobacterium species NRC-1."

RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE ARCHAEL BETA CHAIN IS A REGULATORY SUBUNIT.

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate + H(+) (out).

CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.

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CC EMBL: AE005102; AAG20276.1;

DR InterPro: IPR000793; ATPase_a/bC.

DR InterPro: IPR004100; ATPase_a/bN.

DR InterPro: IPR00194; ATPase_a/bcentre.

DR Pfam: PF00006; ATP-synt_ab.1.

DR Pfam: PF00306; ATP-synt_ab.C.1.

DR Pfam: PF02874; ATP-synt_ab.N.1.

DR TIGRFAMs: TIGR01041; ATP_syn_B_arch.1.

DR PROSITE: PS00152; ATPASE_ALPHA_BETA; 1.

DR Hydrolyase; ATP synthetase; Hydrogen ion transport; Complete proteome.

KW SEQUENCE 471 AA; 51957 MW; 12DB1835F0E8A9652 CRC64;

Query Match 72.9%; Score 35; DB 1; Length 471;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIGYD 8
 DB 20 DEPIGYD 26

RESULT 14

ID VATE_HALSA STANDARD; PRT; 471 AA.

AC P25164;

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)
 DE V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit
 GN ATPR.
 OS Halobacterium salinarum.
 OC Archaea: Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=2242;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8; 272-344; 425-444 AND 446-471.
 RX MEDLINE=91378275; PubMed=1832829;
 RA Ihara K., Mukohata Y.;
 RT "The ATP synthase of Halobacterium salinarum (halobium) is an
 RT archaeobacterial type as revealed from the amino acid sequences of its
 RT two major subunits."
 RL Arch. Biochem. Biophys. 286:111-116(1991).
 CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE ARCHAEOAL BETA CHAIN IS A
 CC REGULATORY SUBUNIT.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
 CC H(+) (out).
 CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: X70294; CAA49776.1; -
 DR PIR: S14733; S14733.
 DR InterPro: IPR000793; ATPase_a/b/c.
 DR InterPro: IPR004100; ATPase_a/b/c.
 DR InterPro: IPR000194; ATPase_a/b/c.
 DR Pfam: PF00006; ATP-synt_ab; 1.
 DR Pfam: PF02874; ATP-synt_ab; 1.
 DR Pfam: PF02874; ATP-synt_ab; 1.
 DR TIGRfam: TIGR01041; ATP_syn_B_arch; 1.
 DR PROSITE: PS00152; ATPase_ALPHA_BETA; 1.
 DR Hydrolyase; ATP synthetase; Hydrogen ion transport.
 KM SEQUENCE 471 AA; 51956 MW; 749A55F7B5B34823 CRC64;
 SO
 Query Match 72.9%; Score 35; DB 1; Length 471;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 DAPIGYD 8
 Db 20 DAPIGYD 26
 RESULT 15
 CHIL_BACCI STANDARD: PRT: 699 AA.
 ID CHIL_BACCI
 AC P20533;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Chitinase A1 precursor (EC 3.2.1.14).
 GN CHIA1.
 OS Bacillus circulans.
 OC Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1397;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WL-12;
 RX MEDLINE=90368776; PubMed=2203782;
 RA Watanabe T., Suzuki K., Oyanagi W., Ohnishi K., Tanaka H.;
 RT "Gene cloning of chitinase A1 from Bacillus circulans WL-12 revealed
 RT its evolutionary relationship to Serratia chitinase and to the type
 RT III homology units of fibronectin.";

RL J Biol. Chem. 265:15659-15665(1990).
 RN [12]
 RP MOTAGENESIS.
 RC STRAIN-WL-12;
 RX MEDLINE=93366760; PubMed=8103047;
 RA Watanabe T., Kohori K., Miyashita K., Fujii T., Sakai H.,
 RA Uchida M., Tanaka H.;
 RT "Identification of glutamic acid 204 and aspartic acid 200 in
 RT chitinase A1 of Bacillus circulans WL-12 as essential residues for
 RT chitinase activity."
 RL J Biol. Chem. 268:18567-18572(1993).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
 CC acetyl-D-glucosamine polymers of chitin.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: M57601; AAA81528.1; -
 DR PIR: A38368; A38368.
 DR HSSP: P02751; IFNA.
 DR InterPro: IPR003610; CBM_5_12;
 DR InterPro: IPR001579; Chitinase_18/2.
 DR InterPro: IPR003961; FN.III.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR InterPro: IPR001223; Glyco_hydro_18.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00704; Glyco_hydro_18; 1.
 DR Pfam: PF02839; CBM_5_12; 1.
 DR PRINTS: PR00014; FNTYPEIII.
 DR PRODOM: PD000471; Glyco_hydro_18; 2.
 DR SMART: SM00495; ChitBD3; 1.
 DR SMART: SM00060; FN3; 2.
 DR PROSITE: PS01095; CHITINASE_18; 1.
 DR Hydrolyase; Glycosidase; Chitin degradation; Signal; Repeat.
 KM SIGNAL 1 41
 FT CHAIN 1 41
 FT DOMAIN 42 699 CHITINASE A1.
 FT DOMAIN 42 460 CATALYTIC.
 FT DOMAIN 465 549 FIBRONECTIN TYPE-III (R-1).
 FT DOMAIN 560 644 FIBRONECTIN TYPE-III (R-2).
 FT ACT_SITE 204 204 PROTON DONOR (PROBABLE).
 FT MUTAGEN 200 200 D->N: DECREASE IN ACTIVITY.
 FT MUTAGEN 200 200 D->E: NO CHANGE IN ACTIVITY.
 FT MUTAGEN 204 204 E->D: LOSS OF ACTIVITY.
 SO SEQUENCE 699 AA; 73677 MW; AC7C9B2E2987643 CRC64;
 Query Match 72.9%; Score 35; DB 1; Length 699;
 Best Local Similarity 62.5%; Pred. No. 17;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 1 HDAPIGYD 8
 Db 291 HNAPLMYD 298

Search completed: March 14, 2003, 09:21:17
 Job time: 14 secs

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:20:39 ; Search time 29 Seconds

(without alignments)
56.841 Million cell updates/sec

Title: US-10-007-363-2

Perfect score: 48

Sequence: 1 HDAPICVD 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	39	81.2	652	3 060070	060070 schizosacch
2	39	81.2	869	13 042126	042126 xenopus lae
3	37	77.1	493	5 044320	044320 hippocamla
4	37	77.1	695	11 091W8	091W8 ratius norv
5	35	72.9	171	2 09F5F3	09F5F3 agrobacteri
6	35	72.9	180	10 09LZG9	09LZG9 arabidopsi
7	35	72.9	199	2 09R6J9	09R6J9 agrobacteri
8	35	72.9	199	16 08U626	08U626 agrobacteri
9	35	72.9	218	16 08XHB1	08XHB1 clostridium
10	35	72.9	371	5 09NAMS	09NAMS caenorhabdi
11	35	72.9	437	3 074958	074958 schizosacch
12	35	72.9	457	6 09XSH5	09XSH5 salimiri bol
13	35	72.9	457	6 09XT11	09XT11 actus nancy
14	35	72.9	457	6 09X512	09X512 saguinus oe
15	35	72.9	457	6 095L05	095L05 cercopithec
16	34.5	71.9	553	10 049931	049931 pisum sativ

17	34	70.8	177	2 09EUW4	09EUW4 listeria in
18	34	70.8	205	16 09ZLM9	09ZLM9 helicobacte
19	34	70.8	245	2 09JH02	09JH02 streptomyce
20	34	70.8	285	3 09P350	09P350 neurospora
21	34	70.8	304	12 039253	039253 equine herp
22	34	70.8	323	2 09AG01	09AG01 shigella fl
23	34	70.8	326	5 018648	018648 caenorhabdi
24	34	70.8	335	5 09W2V4	09W2V4 drosophila
25	34	70.8	387	5 09VZX1	09VZX1 drosophila
26	34	70.8	392	16 08YLF2	08YLF2 anabaena sp
27	34	70.8	401	2 07476	07476 escherichia
28	34	70.8	411	16 097L71	097L71 clostridium
29	34	70.8	424	2 08VSQ3	08VSQ3 shigella fl
30	34	70.8	458	5 09VF23	09VF23 drosophila
31	34	70.8	463	10 09AU48	09AU48 dioscorea e
32	34	70.8	470	2 0990R0	0990R0 shigella fl
33	34	70.8	470	2 08VSJ7	08VSJ7 shigella fl
34	34	70.8	483	16 08ZAN2	08ZAN2 yersinia pe
35	34	70.8	484	2 0990F4	0990F4 shigella fl
36	34	70.8	484	2 08VSL8	08VSL8 shigella fl
37	34	70.8	484	2 08VSL8	08VSL8 shigella fl
38	34	70.8	550	5 08SQW5	08SQW5 shigella fl
39	34	70.8	556	10 094135	094135 oryza sativ
40	34	70.8	668	17 08TX28	08TX28 methanopyru
41	34	70.8	675	16 08ZG01	08ZG01 yersinia pe
42	34	70.8	677	16 09HYC7	09HYC7 pseudomonas
43	34	70.8	677	16 08ZNM4	08ZNM4 salmonella
44	34	70.8	677	16 08ZNM4	08ZNM4 salmonella
45	34	70.8	677	16 08ZSC3	08ZSC3 salmonella

ALIGNMENTS

RESULT 1

ID	060070	PRELIMINARY:	PRT:	652 AA.
AC	060070:			
DT	01-AUG-1998 (TREMBLrel. 07, Created)			
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Hypothetical 74.3 kDa protein C1361.08C in chromosome II.			
GN	SPC1361.08C.			
OS	Schizosaccharomyces pombe (Fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
CC	Schizosaccharomycetes.			
OX	NCBI_TaxID=4896;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=972;			
RA	Lyne M., Wood V., Rajandream M.A., Barrell B.G., Badcock K.,			
RA	Churcher C.M., (Apr-1998) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: SOME TO HUMAN ASH2L.			
DR	EMBL: AL022600; CAA18661.1; -			
DR	InterPro: IPR003878; SPRY domain.			
DR	InterPro: IPR003877; SPRY receptor.			
DR	InterPro: IPR001965; Znf_PHD.			
DR	Pfam: PF00622; SPRY; 1.			
DR	SMART: SM00249; PHD; 1.			
DR	SMART: SM00449; SPRY; 1.			
SK	Hypothetical protein.			
QW	SEQUENCE 652 AA; 74252 MW; 998E783EC8BD0360 CRC64;			

Query Match 81.2%; Score 39; DB 3; Length 652;

Best Local Similarity 85.7%; Pred. No. 31;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPICVD 8

DB 419 DAPICVD 425

```

RESULT 2
ID 042126 PRELIMINARY; PRT; 869 AA.
AC 042126;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Vitellogenin receptor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
OX NCB1
RN NCB1
RP NCB1
RC TISSUE=OOCYTE;
RA Okabayashi K.;
RT Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
RL [2]
RX MEDLINE-96295501; PubMed-8702402;
RA Okabayashi K., Shoji H., Nakamura T., Hashimoto O., Asashima M.,
RA Sugino H.;
RT "CDNA Cloning and Expression of the Xenopus laevis Vitellogenin
RT Receptor.";
RL Biochem. Biophys. Res. Commun. 224:406-413(1996).
EMBL: AB006906; BAA22145.1; -
DR HSSP: P01150; IAUJ.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF Ca.
DR InterPro: IPR000033; Ldl_receptor_rep.
DR InterPro: IPR002172; Ldl_receptor_A.
DR Pfam: PF00057; Ldl_recept_a; 8.
DR Pfam: PF00058; Ldl_recept_b; 5.
DR PRINTS: PR00261; LDLRECEPTOR.
DR SMART: SM00179; EGF_CA.1.
DR SMART: SM00001; EGF_like; 2.
DR SMART: SM00192; LDLA; 8.
DR SMART: SM00135; LY; 5.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_2.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS01209; LDLRA_1; 8.
DR PROSITE: PS50068; LDLRA_2; 8.
DR Calcium-binding; EGF-like domain; Glycoprotein; Receptor; Repeat.
SQ SEQUENCE 869 AA; 96378 MW; A57A3B34072EB517 CRC64;

Query Match 81.2%; Score 39; DB 13; Length 869;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
DB 371 HDLPICYE 378

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RN [1]
RP SEQUENCE FROM N.A.
RA Burke W.D., Malik H.S., Eickbush T.H.;
RT "R1 and R2 Provide an Estimate of the Age and Stability of
RT Retrotransposons.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF015816; AAB94040.1;
DR InterPro: IPR000477; RTase.
DR Pfam: PF00078; FVL; 1.
KW RNA-directed DNA polymerase.
FT NON_TER
SQ SEQUENCE 493 AA; 55882 MW; 19F76B92C636B9C9 CRC64;

Query Match 77.1%; Score 37; DB 5; Length 493;
Best Local Similarity 71.4%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPIGY 7
DB 159 HDVPGY 165

RESULT 4
ID 091WX8 PRELIMINARY; PRT; 695 AA.
AC 091WX8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Voltage-gated calcium channel pore forming subunit Cav1.3alpha1
DE (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN NCB1
RP NCB1
RC TISSUE=SPRAGUE-DAWLEY; TISSUE=SUPERIOR CERVICAL GANGLIA;
RX MEDLINE-21380268; PubMed-11487617;
RA Xu W., Lipscombe D.;
RT "Neuronal Ca(V)1.3alpha(1) L-type channels activate at relatively
RT hyperpolarized membrane potentials and are incompletely inhibited by
RT dihydropyridines.";
RL J. Neurosci. 21:5944-5951(2001).
DR EMBL: AF370010; AAK72960.1; -
FT NON_TER
SQ SEQUENCE 695 AA; 79034 MW; B9A5A1CE11FE7D32 CRC64;

Query Match 77.1%; Score 37; DB 11; Length 695;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DAPIGYD 8
DB 429 DSPICYD 435

RESULT 5
ID 09F5F3 PRELIMINARY; PRT; 171 AA.
AC 09F5F3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE RIOR197 protein.
GN RIORF97.
OS Agrobacterium rhizogenes.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCB1_TaxID=359;
RN NCB1
RP SEQUENCE FROM N.A.

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RC STRAIN-MAFF03-01724;
RA Moriguchi K., Maeda Y., Satou M., Satuti N., Kataoka M., Tanaka N.,
RA Yoshida K.;
RT "The complete nucleotide sequence of a Ri (root inducing) plasmid
RT indicates its chimerical structure between Ti and Sym plasmids.";
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF03-01724;
RA Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.;
RT "Analysis of unique variable region of a plant root inducing plasmid,
RT pRI1724, by the construction of its physical map and library.";
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF03-01724;
RA Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.;
RT "Genome structure of Ri plasmid (1): Construction of linking library
RT and physical map of pRI1724 in Japanese Agrobacterium.";
RL Nucleic Acids Symp. Ser. 39:189-190(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF03-01724;
RX MEDLINE=20241294; PubMed=10780382;
RA Maeda Y., Moriguchi K., Kataoka M., Satou M., Satuti N., Tanaka N.,
RA Yoshida K.;
RT "Genome structure of Ri plasmid (1): Sequencing analysis of T-DNA and
RT its flanking regions of pRI1724 in Japanese Agrobacterium
RT rhizogenes.";
RL Nucleic Acids Symp. Ser. 42:67-68(1999).
DR EMBL: AP002086; BAB16216.1; -.
KW Plasmid.
SQ SEQUENCE 171 AA; 18295 MW; 730160B1FD0E0F52 CRC64;

Query Match 72.9%; Score 35; DB 2; Length 171;
Best Local Similarity 71.4%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
Db 99 DGPVGYD 105

RESULT 6
Q9LZG9 PRELIMINARY; PRT; 180 AA.
ID Q9LZG9;
AC Q9LZG9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE Hypothetical 19.8 kDa protein.
GN T28A8.70.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Purrelle B., Bouty M., Goffeau A., Mewes H.W., Rudd S., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL162691; CAB83150.1; -.
KW Hypothetical protein.
SQ SEQUENCE 180 AA; 19838 MW; 42A91B9998E18CF6 CRC64;

Query Match 72.9%; Score 35; DB 10; Length 180;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 HDAPIGYD 8
Db 38 HDPIGYD 45

RESULT 7
Q9R6J9 PRELIMINARY; PRT; 199 AA.
ID Q9R6J9;
AC Q9R6J9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TIORF60 protein.
GN TIORF60.
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF301001;
RX MEDLINE=20184752; PubMed=10721727;
RA Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,
RA Katoh A., Yoshida K.;
RT "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF301001;
RX MEDLINE=98193120; PubMed=9524202;
RA Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
RT "Novel structural difference between nopaline- and octopine- type
RT trb/trai and rep gene clusters of a new Ti plasmid pTi-SAKURA.";
RL Biochim. Biophys. Acta 1396:177(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF301001;
RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
RT "Genome structure of pTi-SAKURA (I): Strategy for DNA sequencing of a
RT Japanese cherry-Ti plasmid.";
RL Nucleic Acids Symp. Ser. 37:159-160(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF301001;
RA Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.;
RT "Genome structure of pTi-SAKURA (II): Characteristics of T-DNA.";
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF301001;
RA Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;
RT "Genome structure of pTi-SAKURA (IV): Characteristics of tra region.";
RL Nucleic Acids Symp. Ser. 39:187-188(1998).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN-MAFF301001;
RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
RT "Genome structure of pTi-SAKURA (V): Complete nucleotide sequence of
RT plasmid pTi-SAKURA's vir region in Agrobacterium tumefaciens.";
RL Nucleic Acids Symp. Ser. 39:265-266(1998).
DR EMBL: AB016260; BAA87685.1; -.
KW Plasmid.
SQ SEQUENCE 199 AA; 21186 MW; 8488087EED322126 CRC64;

Query Match 72.9%; Score 35; DB 2; Length 199;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DAPIGYD 8
Db 11:111

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DB 127 DGPVGYD 133

RESULT 8

08U626 PRELIMINARY: PRT: 199 AA.

AC 08U626: 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

GN Agrobacterium tumefaciens (strain C58 / ATCC 33970).

OC Plasmid pTIC58.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Rhizobiaceae; Rhizobium.

OX NCBI_TaxID=176299;

RP SEQUENCE FROM N.A.

RA MEDLINE-21608550; PubMed-11743193;

RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitaajima J.P.,

RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,

RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boye D. Sr.,

RA Chapman P., Clendenning J., Deatherage G., Gilliet W., Grant C.,

RA Kutayavir T., Levy R., Li M.-J., McCelland E., Palmeri A., Gordon D.,

RA Raymond C., Kouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,

RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,

RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

RA Nester E.W.;

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens C58."

RL Science 294:2317-2323(2001).

OX [12]

RP SEQUENCE FROM N.A.

RA MEDLINE-21608551; PubMed-11743194;

RA Goodner B., Hunkle G., Gattung S., Miller N., Blanchard M.,

RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,

RA Hounzel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,

RA Wollam C., Allinger M., Doughy D., Scott C., Lapps C., Markelz B.,

RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,

RA Cleto C., Slater S.;

RT "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."

RL Science 294:2323-2328(2001).

DR EMBL: AE009430; AAL46345.1; -

DR EMBL: AE007938; AAK91070.1; -

KW Hypothetical protein; Plasmid; Complete proteome.

SO SEQUENCE 199 AA; 21117 MW; DBD89FF3478DD04A CRC64;

Query Match 72.9%; Score 35; DB 16; Length 199;

Best Local Similarity 71.4%; Pred. No. 51;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIGYD 8

DB 127 DGPVGYD 133

RESULT 9

08XHBI PRELIMINARY: PRT: 218 AA.

AC 08XHBI: 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

GN Hypothetical protein CPE2574.

OC Clostridium perfringens.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;

OC Clostridiales; Clostridiaceae; Clostridium.

OX NCBI_TaxID=1502;

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=13 / TYPE A;

RX PubMed-11792842;

RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,

RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;

RT "Complete genome sequence of Clostridium perfringens, an anaerobic flesh-eater."

RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).

DR EMBL: AP003194; BAB82280.1; -

KW Hypothetical protein; Complete proteome.

SO SEQUENCE 218 AA; 25146 MW; 7B7AA90FBEB4DC3F CRC64;

Query Match 72.9%; Score 35; DB 16; Length 218;

Best Local Similarity 71.4%; Pred. No. 57;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HDAPGY 7

DB 101 HSAPEGY 107

RESULT 10

09NAMS PRELIMINARY: PRT: 371 AA.

AC 09NAMS: 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE Y105C5B.16 protein.

GN Y105C5B.16.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Pelodermidae; Caenorhabditis.

OX NCBI_TaxID=6239;

RP SEQUENCE FROM N.A.

RA McMurray A.A.;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN [12]

RP SEQUENCE FROM N.A.

RA MEDLINE-99069613; PubMed-9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for investigating biology."

RL Science 282:2012-2018(1998).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.

DR EMBL: AL110479; CAB54361.1; -

DR InterPro: IPR001175; Neur-channel.

DR Pfam: PF02931; Neur_chan_LBD; 1.

DR PRINTS: PR00252; NRIONCHANNEL.

DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.

KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.

SO SEQUENCE 371 AA; 43547 MW; 25A835F23D341D92 CRC64;

Query Match 72.9%; Score 35; DB 5; Length 371;

Best Local Similarity 85.7%; Pred. No. 1e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 DAPIGYD 8

DB 59 DLPIGYD 65

RESULT 11

074958 PRELIMINARY: PRT: 437 AA.

AC 074958: 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE Hypothetical serine-rich protein.

GN SPC736.12C.

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OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-972H-;
RA Wood V., Rajandream M.A., Barrell B.G., Murphy L., Harris D.,
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL023705; CAA19276.2;
SQ SEQUENCE 437 AA; 48702 MW; E0981EDE494A88A8 CRC64;

Query Match
Best Local Similarity 72.9%; Score 35; DB 3; Length 437;
Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HDAPIG 6
Db 76 HDAPIG 81

RESULT 12
O9XSH5 PRELIMINARY; PRT; 457 AA.
AC O9XSH5;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE FK506-binding protein FKBP51.
OS Saimiri boliviensis (Bolivian squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.
OX NCBI_TaxID=27679;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-20539274; PubMed-11089542;
RA Denny W.B., Valentine D.L., Reynolds P.D., Smith D.F., Scammell J.G.;
RT "Squirrel Monkey Immunophilin FKBP51 Is a Potent Inhibitor of
RT Glucocorticoid Receptor Binding."
RL Endocrinology 141:4107-4113(2000).
DR EMBL; AF140759; AAD32678.1;
DR HSSP; P27124; 1ROT.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00254; FKBP; 2.
DR Pfam; PF00515; TPR; 2.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 2.
SQ SEQUENCE 457 AA; 51169 MW; DEF9E1D81F7759A8 CRC64;

Query Match
Best Local Similarity 72.9%; Score 35; DB 6; Length 457;
Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIG 8
Db 196 HDIPIGID 203

RESULT 13
O9XT11 PRELIMINARY; PRT; 457 AA.
ID O9XT11;
AC O9XT11;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE FK506-binding protein FKBP51.
GN FKBP51.
OS Aotus nancymae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

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OX NCBI_TaxID=37293;
RN (1)
RP SEQUENCE FROM N.A.
RA Scammell J.G., Valentine D.L.;
RT "Cloning and expression of owl monkey FKBP51 cDNA."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF141937; AAD33882.2;
DR HSSP; P27124; 1ROT.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00254; FKBP; 2.
DR Pfam; PF00515; TPR; 2.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 2.
SQ SEQUENCE 457 AA; 51297 MW; 56B7EBC6E290486 CRC64;

Query Match
Best Local Similarity 72.9%; Score 35; DB 6; Length 457;
Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIG 8
Db 196 HDIPIGID 203

RESULT 14
O9XS12 PRELIMINARY; PRT; 457 AA.
ID O9XS12;
AC O9XS12;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE FK506-binding protein FKBP51.
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=9490;
RN (1)
RP SEQUENCE FROM N.A.
RA Scammell J.G., Valentine D.L.;
RT "Cloning and expression of cotton-top tamarin FKBP51 cDNA."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF143809; AAD33918.2;
DR HSSP; P27124; 1ROT.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00254; FKBP; 2.
DR Pfam; PF00515; TPR; 2.
DR PROSITE; PS00453; FKBP_PPIASE_1; 1.
DR PROSITE; PS00454; FKBP_PPIASE_2; 1.
DR PROSITE; PS50059; FKBP_PPIASE_3; 2.
SQ SEQUENCE 457 AA; 51116 MW; F2M4E2A2B6658302 CRC64;

Query Match
Best Local Similarity 72.9%; Score 35; DB 6; Length 457;
Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIG 8
Db 196 HDIPIGID 203

RESULT 15
O9SL05 PRELIMINARY; PRT; 457 AA.
ID O9SL05;
AC O9SL05;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE FK506-binding protein FKBP51.
OS Ceropithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea;
 OC Cercopithecoidea: Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Denny W.B., Scammell J.G.;
 RT "African Green Monkey Immunophilin FKBP51."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY044168; AAK95405.1;
 DR InterPro: IPR001179; FKBP_PPIase.
 DR InterPro: IPR001440; TPR.
 DR Pfam: PF00254; FKBP_2.
 DR Pfam: PF00515; TPR_2.
 DR PROSITE: PS00454; FKBP_PPIase_2; UNKNOWN_1.
 DR PROSITE: PS50059; FKBP_PPIase_3; 2.
 DR PROSITE: 457 AA; 51095 MW; 9CB4CA338CF75144 CRC64;
 SQ SEQUENCE

Query Match 72.9%; Score 35; DB 6; Length 457;
 Best local Similarity 75.0%; Pred. NO. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HDAPIGYD 8
 |||||
 Db 196 HDIPIGID 203

Search completed: March 14, 2003, 09:23:04
 Job time : 32 secs

10/007363

L1 FILE 'REGISTRY' ENTERED AT 12:42:49 ON 14 MAR 2003
24 S HDAPIGYD/SQSP

L2 FILE 'HCAPLUS' ENTERED AT 12:43:08 ON 14 MAR 2003
16 S L1

L2 ANSWER 1 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2003:129399 HCAPLUS
DOCUMENT NUMBER: 138:164734
TITLE: Animal model system for squamous cell carcinoma
based on increased expression of recombinant
protein kinase C.epsilon.
INVENTOR(S): Verma, Ajit K.; Reddig, Peter J.; Jansen, Aaron
P.
PATENT ASSIGNEE(S): Wisconsin Alumni Research Foundation, USA
SOURCE: U.S., 16 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6521815	B1	20030218	US 2001-772647	20010130
US 2003051258	A1	20030313	US 2002-228931	20020827

PRIORITY APPLN. INFO.: US 2001-772647 A1 20010130

AB Non-human mammalian animals having a higher epidermal expression level of protein kinase C.epsilon. than their wild-type counterparts are phenotypically distinguished from wild-type animals in that the animals induced to develop tumors in a chem. initiation/promotion protocol are suppressed for subsequent papilloma development but are susceptible to developing squamous cell carcinoma and metastatic squamous cell carcinoma. The animals are advantageously used in methods for screening putative agents for altering the susceptibility, development and progression of squamous cell carcinoma and metastatic squamous cell carcinoma and have further com. value as tools for investigating the development of metastatic disease.

IT 497267-31-9
RL: ADV (Adverse effect, including toxicity); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; animal model system for squamous cell carcinoma based on increased expression of recombinant protein kinase C.epsilon.)

REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 2 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2003:7668 HCAPLUS
DOCUMENT NUMBER: 138:164520
TITLE: Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
AUTHOR(S): Okazaki, Y.; Furuno, M.; Kasukawa, T.; Adachi, J.; Bono, H.; Kondo, S.; Nikaido, I.; Osato, N.;

Saito, R.; Suzuki, H.; Yamanaka, I.; Kiyosawa, H.; Yagi, K.; Tomaru, Y.; Hasegawa, Y.; Nogami, A.; Schoenbach, C.; Gojobori, T.; Baldarelli, R.; Hill, D. P.; Bult, C.; Hume, D. A.; Quackenbush, J.; Schriml, L. M.; Kanapin, A.; Matsuda, H.; Batalov, S.; Beisel, K. W.; Blake, J. A.; Bradt, D.; Brusic, V.; Chothia, C.; Corbani, L. E.; Cousins, S.; Dalla, E.; Dragani, T. A.; Fletcher, C. F.; Forrest, A.; Frazer, K. S.; Gaasterland, T.; Gariboldi, M.; Gissi, C.; Godzik, A.; Gough, J.; Grimmond, S.; Gustincich, S.; Hirokawa, N.; Jackson, I. J.; Jarvis, E. D.; Kanai, A.; Kawaji, H.; Kawasawa, Y.; Kedzierski, R. M.; King, B. L.; Konagaya, A.; Kurochkin, I. V.; Lee, Y.; Lenhard, B.; Lyons, P. A.; Maglott, D. R.; Maltais, L.; Marchionni, L.; McKenzie, L.; Miki, H.; Nagashima, T.; Numata, K.; Okido, T.; Pavan, W. J.; Pertea, G.; Pesole, G.; Petrovsky, N.; Pillai, R.; Pontius, J. U.; Qi, D.; Ramachandran, S.; Ravasi, T.; Reed, J. C.; Reed, D. J.; Reid, J.; Ring, B. Z.; Ringwald, M.; Sandelin, A.; Schneider, C.; Sempere, C. A. M.; Setou, M.; Shimada, K.; Sultana, R.; Takenaka, Y.; Taylor, M. S.; Teasdale, R. D.; Tomita, M.; Verardo, R.; Wagner, L.; Wahlestedt, C.; Wang, Y.; Watanabe, Y.; Wells, C.; Wilming, L. G.; Wynshaw-Boris, A.; Yanagisawa, M.; Yang, I.; Yang, L.; Yuan, Z.; Zavolan, M.; Zhu, Y.; Zimmer, A.; Carninci, P.; Hayatsu, N.; Hirozane-Kishikawa, T.; Konno, H.; Nakamura, M.; Sakazume, N.; Sato, K.; Shiraki, T.; Waki, K.; Kawai, J.; Aizawa, K.; Arakawa, T.; Fukuda, S.; Hara, A.; Hashizume, W.; Imotani, K.; Ishii, Y.; Itoh, M.; Kagawa, I.; Miyazaki, A.; Sakai, K.; Sasaki, D.; Shibata, K.; Shinagawa, A.; Yasunishi, A.; Yoshino, M.; Waterston, R.; Lander, E. S.; Rogers, J.; Birney, E.; Hayashizaki, Y.

CORPORATE SOURCE:

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
Nature (London, United Kingdom) (2002), 420(6915), 563-573

SOURCE:

CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER:

Nature Publishing Group

DOCUMENT TYPE:

Journal

LANGUAGE:

English

AB Only a small proportion of the mouse genome is transcribed into mature mRNA transcripts. There is an international collaborative effort to identify all full-length mRNA transcripts from the mouse, and to ensure that each is represented in a phys. collection of clones. The manual annotation of 60,770 full-length mouse cDNA sequences is now reported. These are clustered into 33,409 'transcriptional units', contributing 90.1% of a newly established mouse transcriptome database. Of these transcriptional units, 4258 are new protein-coding and 11,665 are new non-coding messages, indicating that non-coding RNA is a major component of the

transcriptome. Forty-one percent of all transcriptional units showed evidence of alternative splicing. In protein-coding transcripts, 79% of splice variations altered the protein product. Whole-transcriptome analyses resulted in the identification of 2431 sense-antisense pairs. The present work, completely supported by phys. clones, provides the most comprehensive survey of a mammalian transcriptome so far, and is a valuable resource for functional genomics. The cDNA sequences are deposited in GenBank/EMBL/DBJ under accession nos. AK002213-AK021412, AK027261-AK054560, AK075567-AK090394, and AK117103-AK117104. [This abstr. record is one of thirty records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints].

IT **493572-11-5**, GenBank BAC31430

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; anal. of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs)

L2 ANSWER 3 OF 16 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:869420 HCAPLUS

DOCUMENT NUMBER: 137:363111

TITLE: Psiepsilon RACK peptide composition and method for protection against tissue damage due to ischemia

INVENTOR(S): Mochly-Rosen, Daria

PATENT ASSIGNEE(S): USA

SOURCE: U.S. Pat. Appl. Publ., 17 pp.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002168354	A1	20021114	US 2001-7363	20011109
PRIORITY APPLN. INFO.:			US 2000-247830P	P 20001110

AB A method of reducing damage to cells and tissue caused by an ischemic or hypoxic event is disclosed. The method includes administering to the cell or tissue, either in vivo or ex vivo, .psi..epsilon.RACK peptide. The peptide can be administered before, during or after the ischemic or hypoxic event.

IT **207111-98-6**

RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(.psi..epsilon.-RACK peptide compn. and method for protection against tissue damage due to ischemia)

L2 ANSWER 4 OF 16 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:777625 HCAPLUS

DOCUMENT NUMBER: 137:289003

TITLE: Pseudo-epsilon RACK (.psi..epsilon.RACK) peptide composition and method for protection against heart tissue damage due to ischemia

INVENTOR(S): Mochly-Rosen, Daria

PATENT ASSIGNEE(S): The Board of Trustees of the Leland Stanford Junior University, USA

10/007363

SOURCE: PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002078600	A2	20021010	WO 2001-US51600	20011109
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				

PRIORITY APPLN. INFO.: US 2000-274830P P 20001110
AB A method of reducing damage to cells and tissue in heart caused by an ischemic or hypoxic event is disclosed. The method includes administering to the cell or tissue, either in vivo or ex vivo, .psi..epsilon.RACK peptide. The peptide can be administered before, during or after the ischemic or hypoxic event.

IT 207111-98-6
RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (pseudo-epsilon RACK (.psi..epsilon.RACK) peptide compn. and method for protection against heart tissue damage due to ischemia)

L2 ANSWER 5 OF 16 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:616256 HCAPLUS

DOCUMENT NUMBER: 137:181594

TITLE: Dominant-negative variants of human protein kinases that inhibit the phosphorylation activity of their active enzyme isoforms

INVENTOR(S): Levine, Zurit; Bernstein, Jeanne

PATENT ASSIGNEE(S): Compugen Ltd., Israel

SOURCE: U.S. Pat. Appl. Publ., 170 pp., Cont.-in-part of U.S. Ser. No. 724,676.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002110811	A1	20020815	US 2001-771161	20010126
PRIORITY APPLN. INFO.:				
			IL 2000-135619	A 20000512
			IL 2000-136776	A 20000615
			US 2000-724676	A2 20001128

AB The present invention concerns 91 nucleic acid sequences and amino acid sequences of variants of various human kinases, i.e. of sequences which inhibit activity of kinases in a dominant manner. The variants lack a domain or region required for phosphorylation, and thus may be dominant-neg. kinases obtained by alternative splicing of known original sequences of the kinase genes. The novel dominant-neg. kinase variants of the invention are not merely artificially truncated forms, fragments or mutations of known genes, but rather novel sequences which naturally occur within the body of individuals. The invention also concerns pharmaceutical compns. and

detection methods using these sequences.

IT 449216-82-4

RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; dominant-neg. variants of human protein kinases that inhibit the phosphorylation activity of their active enzyme isoforms)

IT 449225-92-7

RL: PRP (Properties)
(unclaimed protein sequence; dominant-neg. variants of human protein kinases that inhibit the phosphorylation activity of their active enzyme isoforms)

L2 ANSWER 6 OF 16 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:539800 HCAPLUS

DOCUMENT NUMBER: 137:104169

TITLE: Use of an invertebrate system to identify modulators of the insulin signal transduction chain and the identification of effectors of insulin signal transduction

INVENTOR(S): Seidel-Dugan, Cynthia; Ferguson, Kimberly Carr; Kidd, Thomas

PATENT ASSIGNEE(S): Exelixis, Inc., USA

SOURCE: PCT Int. Appl., 232 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002055664	A2	20020718	WO 2002-US1048	20020111
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			

PRIORITY APPLN. INFO.:

US 2001-261226P	P	20010112
US 2001-261303P	P	20010112
US 2001-261304P	P	20010112
US 2001-261335P	P	20010112
US 2001-261336P	P	20010112
US 2001-261361P	P	20010112
US 2001-261456P	P	20010112
US 2001-261457P	P	20010112
US 2001-261458P	P	20010112
US 2001-261459P	P	20010112
US 2001-261461P	P	20010112
US 2001-261518P	P	20010112
US 2001-261531P	P	20010112
US 2001-261532P	P	20010112

10/007363

US 2001-261589P P 20010112
US 2001-261590P P 20010112
US 2001-261694P P 20010112
US 2001-261695P P 20010112
US 2001-261697P P 20010112

AB A method of using invertebrate test systems to identify modulators of the insulin signal transduction pathway are described. These proteins are therapeutic targets for disorders assocd. with defective insulin receptor signaling. Methods for identifying modulators of ISM, comprising screening for agents that modulate the activity of ISM are provided. The genes for these regulators are then used to clone their human orthologs. Factors affecting the function of the *Caenorhabditis elegans* insulin receptor encoded by the *daf-2* gene were screened for by their ability to revert a mutation leading to the dauer state. A *Drosophila* screen using a P-element carrying a GAL4-regulated promoter was used to identify external suppressors of a mutation in the *Dinr* gene. CDNA and protein sequences of human orthologs of these genes and proteins are presented.

IT 442703-09-5

RL: PRP (Properties)

(unclaimed protein sequence; use of an invertebrate system to identify modulators of the insulin signal transduction chain and the identification of effectors of insulin signal transduction)

L2 ANSWER 7 OF 16 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:2517 HCAPLUS

DOCUMENT NUMBER: 137:237523

TITLE: Molecular transporters for peptides: delivery of a cardioprotective .epsilon.PKC agonist peptide into cells and intact ischemic heart using a transport system, R7

AUTHOR(S): Chen, Leon; Wright, Lee R.; Chen, Che-Hong; Oliver, Steven F.; Wender, Paul A.; Mochly-Rosen, Daria

CORPORATE SOURCE: Department of Molecular Pharmacology, Stanford University School of Medicine, Stanford, CA, 94305-5174, USA

SOURCE: Chemistry & Biology (2001), 8(12), 1123-1129
CODEN: CBOLE2; ISSN: 1074-5521

PUBLISHER: Elsevier Science Ltd.

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Background: Recently, we reported a novel oligoguanidine transporter system, polyarginine (R7), which, when conjugated to spectroscopic probes (e.g., fluorescein) and drugs (e.g., cyclosporin A), results in highly water-sol. conjugates that rapidly enter cells and tissues. We report herein the prepn. of the first R7 peptide conjugates and a study of their cellular and organ uptake and functional activity. The octapeptide .psi..epsilon.RACK was selected for this study as it is known to exhibit selective .epsilon. protein kinase C isoenzyme agonist activity and to reduce ischemia-induced damage in cardiomyocytes. However, .psi..epsilon.RACK is not cell-permeable. Results: Here we show that an R7-.psi..epsilon.RACK conjugate readily enters cardiomyocytes, significantly outperforming .psi..epsilon.RACK conjugates of the transporters derived from HIV Tat and from Antennapedia. Moreover, R7-.psi..epsilon.RACK conjugate reduced

ischemic damage when delivered into intact hearts either prior to or after the ischemic insult. Conclusions: Our data suggest that R7 converts a peptide lead into a potential therapeutic agent for the ischemic heart.

IT 207111-98-6D, conjugates 459146-74-8

459146-76-0 459146-77-1 459146-78-2

459146-82-8 459146-86-2 459146-88-4

RL: PAC (Pharmacological activity); PKT (Pharmacokinetics); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(delivery of cardioprotective .epsilon.PKC agonist peptide into cells and intact ischemic heart using polyarginine transport system)

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 8 OF 16 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:763058 HCAPLUS

DOCUMENT NUMBER: 135:327323

TITLE: NMDA receptor complexes for diagnostic and therapeutic use

INVENTOR(S): Grant, Seth Garran Niels; Husi, Holger

PATENT ASSIGNEE(S): The University Court of the University of Edinburgh, UK

SOURCE: PCT Int. Appl., 202 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001077170	A2	20011018	WO 2001-GB1570	20010406
WO 2001077170	A3	20020328		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1272517	A2	20030108	EP 2001-917331	20010406
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR			
PRIORITY APPLN. INFO.:			GB 2000-8321	A 20000406
			WO 2001-GB1570	W 20010406
AB	The present invention provides multi-protein complexes, and sub-complexes thereof, and methods of producing the same. Preferably, the complexes comprise an NMDA receptor. The present invention further provides methods of identifying a compd. for treating disorders and conditions assocd. with dysfunction of NMDA receptors in the central nervous system. Addnl., there are provided methods of diagnosing or aiding diagnosis of disorders and			

10/007363

conditions assocd. with dysfunction of NMDA receptors in the central nervous system.

IT 148294-93-3 367633-06-5, Protein (mouse clone P16054)

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)

(amino acid sequence; NMDA receptor complexes for diagnostic and therapeutic use)

L2 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2000:910579 HCAPLUS

DOCUMENT NUMBER: 134:160633

TITLE: Evidence for functional role of .epsilon.PKC isozyme in the regulation of cardiac Ca²⁺ channels

AUTHOR(S): Hu, Keli; Mochly-Rosen, Daria; Boutjdir, Mohamed

CORPORATE SOURCE: Molecular and Cellular Cardiology Program, Veterans Affairs New York Harbor Healthcare System, Brooklyn, NY, 11209, USA

SOURCE: American Journal of Physiology (2000), 279(6, Pt. 2), H2658-H2664

CODEN: AJPHAP; ISSN: 0002-9513

PUBLISHER: American Physiological Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Limited information is available regarding the effects of protein kinase C (PKC) isoenzyme(s) in the regulation of L-type Ca²⁺ channels due to lack of isoenzyme-selective modulators. To dissect the role of individual PKC isoenzymes in the regulation of cardiac Ca²⁺ channels, we used the recently developed novel peptide activator of the .epsilon.PKC, .epsilon.V1-7, to assess the role of .epsilon.PKC in the modulation of L-type Ca²⁺ current (I_{Ca,L}). Whole cell I_{Ca,L} was recorded using patch-clamp technique from rat ventricular myocytes. Intracellular application of .epsilon.V1-7 (0.1 .mu.M) resulted in a significant inhibition of I_{Ca,L} by 27.9 .+- 2.2% (P < 0.01, n = 8) in a voltage-independent manner. The inhibitory effect of .epsilon.V1-7 on I_{Ca,L} was completely prevented by the peptide inhibitor of .epsilon.PKC, .epsilon.V1-2 [5.2 .+- 1.7%, not significant (NS), n = 5] but not by the peptide inhibitors of cPKC, .alpha.C2-4 (31.3 .+- 2.9%, P < 0.01, n = 6) or .beta.C2-2 plus .beta.C2-4 (26.1 .+- 2.9%, P < 0.01, n = 5). In addn., the use of a general inhibitor (GF-109203X, 10 .mu.M) of the catalytic activity of PKC also prevented the inhibitory effect of .epsilon.V1-7 on I_{Ca,L} (7.5 .+- 2.1%, NS, n = 6). In conclusion, we show that selective activation of .epsilon.PKC inhibits the L-type Ca channel in the heart.

IT 207111-98-6

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(.epsilon.V1-7 peptide activator of .epsilon.PKC isoenzyme in regulation of cardiac Ca²⁺ channels)

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2003 ACS

10/007363

ACCESSION NUMBER: 1999:728943 HCAPLUS
DOCUMENT NUMBER: 132:44701
TITLE: Sustained in vivo cardiac protection by a
rationally designed peptide that causes
.epsilon. protein kinase C translocation
AUTHOR(S): Dorn, Gerald W., II; Souroujon, Miriam C.;
Liron, Tamar; Chen, Che-Hong; Gray, Mary O.;
Zhou, Hui Zhong; Csukai, Michael; Wu, Guangyu;
Lorenz, John N.; Mochly-Rosen, Daria
CORPORATE SOURCE: Department of Medicine, University of
Cincinnati, Cincinnati, OH, 45167-0590, USA
SOURCE: Proceedings of the National Academy of Sciences
of the United States of America (1999), 96(22),
12798-12803
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Brief periods of cardiac ischemia trigger protection from subsequent
prolonged ischemia (preconditioning). .epsilon. Protein kinase C
(.epsilon.PKC) has been suggested to mediate preconditioning. Here,
we describe an .epsilon.PKC-selective agonist octapeptide,
.psi..epsilon. receptor for activated C-kinase (.psi..epsilon.RACK),
derived from an .epsilon.PKC sequence homologous to its anchoring
protein, .epsilon.RACK. Introduction of .psi..epsilon.RACK into
isolated cardiomyocytes, or its postnatal expression as a transgene
in mouse hearts, increased .epsilon.PKC translocation and caused
cardioprotection from ischemia without any deleterious effects. Our
data demonstrate that .epsilon.PKC activation is required for
protection from ischemic insult and suggest that small mols. that
mimic this .epsilon.PKC agonist octapeptide provide a powerful
therapeutic approach to protect hearts at risk for ischemia.
IT 207111-98-6
RL: BAC (Biological activity or effector, except adverse); BSU
(Biological study, unclassified); THU (Therapeutic use); BIOL
(Biological study); USES (Uses)
(sustained in vivo cardiac protection by a rationally designed
peptide that causes .epsilon. protein kinase C translocation in
transgenic mice)
REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE
FOR THIS RECORD. ALL CITATIONS AVAILABLE
IN THE RE FORMAT

L2 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:268373 HCAPLUS
DOCUMENT NUMBER: 128:317275
TITLE: Isoenzyme-specific peptide activators of protein
kinase C, therapeutic methods to reduce ischemia
injury, compositions, and screening methods
INVENTOR(S): Mochly-Rosen, Daria
PATENT ASSIGNEE(S): Board of Trustees of the Leland Stanford Junior
University, USA
SOURCE: PCT Int. Appl., 47 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9817299	A1	19980430	WO 1997-US18716	19971017
W: CA, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 6165977	A	20001226	US 1997-953033	19971017
PRIORITY APPLN. INFO.:			US 1996-28724P	P 19961018

AB Isoenzyme-specific agonists or activators of .epsilon.PKC are disclosed. The agonists include peptides corresponding to the region of .epsilon.PKC between about amino acids 85 and 92. Also disclosed are therapeutic methods employing such .epsilon.PKC-specific agonists to induce preconditioning and thereby reduce injury due to subsequent ischemia, as well as methods for screening test compds. for .epsilon.PKC-selective agonist properties.

IT 207111-98-6
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
 (isoenzyme-specific peptide activators of protein kinase C, therapeutic methods to reduce ischemia injury, compns., and screening methods)

L2 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1993:423577 HCAPLUS

DOCUMENT NUMBER: 119:23577

TITLE: Sequence and expression of human protein kinase C-.epsilon.

AUTHOR(S): Basta, Patricia; Strickland, Mary Beth; Holmes, William; Loomis, Carson R.; Ballas, Lawrence M.; Burns, David J.

CORPORATE SOURCE: Mol. Biol. Sect., Sphinx Pharm. Corp., Durham, NC, USA

SOURCE: Biochimica et Biophysica Acta (1992), 1132(2), 154-60
 CODEN: BBACAQ; ISSN: 0006-3002

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Two human homologs of protein kinase C-.epsilon. (E1 and E2) were isolated from two distinct cDNA libraries. Sequence comparisons to PKC-.epsilon. cDNAs from several species indicated that each of these human .epsilon. clones contained cloning artifacts. Thus, a composite PKC-.epsilon. (E3) clone was derived from clones E1 and E2. Human PKC-.epsilon. (E3) has an overall sequence identity of 90-92% at the nucleotide level compared to the previously characterized mouse, rat and rabbit clones. At the amino acid level, the deduced human .epsilon. sequence shows a 98-99% identity with the mouse, rat and rabbit sequences. Expression of the human PKC-.epsilon. clone in S19 cells confirmed that the recombinant protein displayed protein kinase C activity and phorbol ester binding activity. The recombinant protein was also recognized by two distinct .epsilon.-specific polyclonal antibodies.

IT 148294-93-3
 RL: PRP (Properties); BIOL (Biological study)
 (amino acid sequence of, complete)

10/007363

L2 ANSWER 13 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1990:453672 HCAPLUS
DOCUMENT NUMBER: 113:53672
TITLE: Cloning and expression and sequence of rat
protein kinase C genes
INVENTOR(S): Ono, Katsutaka; Fujii, Tomoko; Igarashi, Koichi
PATENT ASSIGNEE(S): Takeda Chemical Industries, Ltd., Japan
SOURCE: Jpn. Kokai Tokkyo Koho, 23 pp.
CODEN: JKXXAF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 02000433	A2	19900105	JP 1988-249774	19881005
JP 2771188	B2	19980702		

PRIORITY APPLN. INFO.: JP 1987-252506 19871008
AB The cDNAs encoding the types .delta. and .epsilon. of protein kinase C of rat were cloned and expressed in Escherichia coli. The cloned genes were also transferred to yeast, Bacillus subtilis, and mammalian cell lines for expression. Nucleotide sequences of the cDNAs are given.
IT **116978-12-2**
RL: PRP (Properties)
(amino acid sequence of)

L2 ANSWER 14 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1989:627755 HCAPLUS
DOCUMENT NUMBER: 111:227755
TITLE: Unique substrate specificity and regulatory properties of PKC-.epsilon.: a rationale for diversity
AUTHOR(S): Schaap, Dick; Parker, Peter J.; Bristol, Andrew; Kriz, Ron; Knopf, John
CORPORATE SOURCE: Ludwig Inst. Cancer Res., London, UK
SOURCE: FEBS Letters (1989), 243(2), 351-7
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Protein kinase C (PKC)-.epsilon. was isolated from a murine brain cDNA library. The clone, .lambda.61PKC-.epsilon., encoded a polypeptide of 737 amino acids that is homologous to other PKCs. Northern anal. showed that the 7 kb mRNA for this cDNA is widely expressed. The protein, when expressed in COS-1 cells, displayed phorbol ester-binding activity. However in order to detect the kinase activity of PKC-.epsilon., it was necessary to employ a synthetic peptide substrate based upon the pseudosubstrate site. Subsequent anal. demonstrated that PKC-.epsilon., while showing certain properties characteristic of the PKC family, has a quite distinct substrate specificity and is independent of Ca²⁺.
IT **123514-78-3**
RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of)

L2 ANSWER 15 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1989:52097 HCAPLUS

10/007363

DOCUMENT NUMBER: 110:52097
TITLE: A novel phorbol ester receptor/protein kinase, nPKC, distantly related to the protein kinase C family
AUTHOR(S): Ohno, Shigeo; Akita, Yoshiko; Konno, Yasuhiko; Imajoh, Shinobu; Suzuki, Koichi
CORPORATE SOURCE: Dep. Mol. Biol., Tokyo Metrop. Inst. Med. Sci., Tokyo, 113, Japan
SOURCE: Cell (Cambridge, MA, United States) (1988), 53(5), 731-41
CODEN: CELLB5; ISSN: 0092-8674
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Protein kinase C (PKC)-related cDNA clones encode an 84-kd protein, nPKC. Protein nPKC contains a cysteine-rich repeat sequence homologous to that seen in conventional PKCs (.alpha., .beta..lambda., .beta.II, and .gamma.), which make up a family of 77-78-kd proteins with closely related sequences. Protein nPKC, when expressed in COS cells, confers increased high-affinity phorbol ester receptor activity to intact cells. Antibodies raised against nPKC identified a 90-kd protein in rabbit brain ext. as well as in exts. from COS cells transfected with the cDNA construct. Protein nPKC shows protein kinase activity that is regulated by phospholipid, diacylglycerol, and phorbol ester but is independent of Ca²⁺. The structural and enzymol. characteristics of nPKC clearly distinguish it from conventional PKCs, which until now have been the only substances believed to mediate the various effects of diacylglycerol and phorbol esters. These results suggest an addnl. signaling pathway involving nPKC.
IT 116412-30-7
RL: PRP (Properties)
(amino acid sequence of)

L2. ANSWER 16 OF 16 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1988:585985 HCAPLUS
DOCUMENT NUMBER: 109:185985
TITLE: The structure, expression, and properties of additional members of the protein kinase C family
AUTHOR(S): Ono, Yoshitaka; Fujii, Tomoko; Ogita, Koji; Kikkawa, Ushio; Igarashi, Koichi; Nishizuka, Yasutomi
CORPORATE SOURCE: Cent. Res. Div., Takeda Chem. Ind., Osaka, 532, Japan
SOURCE: Journal of Biological Chemistry (1988), 263(14), 6927-32
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In rat brain, 3 members of the protein kinase C family encoded by cDNAs, termed .delta., .epsilon., and .zeta., were newly identified by mol. cloning and sequence anal. The new members exhibited a common structure that was closely related to but clearly distinct from the 4 members of the family previously isolated having .alpha.-, .beta.I-, .beta.II-, and .gamma.-sequences, although the .zeta.-cDNA available at present did not appear to contain a complete reading frame for protein kinase C. The protein kinase .delta.-, .epsilon.-, and .zeta.-cDNAs all encoded a characteristic

cysteine-rich sequence and protein kinase domain sequence, both of which were highly homologous among the protein kinase C family. However, the new members lacked one of the conserved regions that was present in the .alpha.-, .beta.I, .beta.II-, and .gamma.-sequences. An addnl. cDNA clone termed .epsilon.' was isolated, which was identical with .epsilon.-cDNA except for a short sequence at the 5'-terminal end region. The 2 members having .delta.- and .epsilon.-sequences were expressed in COS 7 cells, and partially purified and characterized. The enzymes having .delta.- and .epsilon.-sequences depended on phospholipid and diacylglycerol for the enzymic activity, but their properties differed slightly from the previously known members of protein kinase C. Northern blot anal. suggested that the new members of protein kinase C exist in the brain and some other tissues.

IT 116978-12-2

RL: PRP (Properties); BIOL (Biological study)
(amino acid sequence of, gene-derived)

E1 THROUGH E18 ASSIGNED

FILE 'REGISTRY' ENTERED AT 12:43:34 ON 14 MAR 2003
L3 18 SEA FILE=REGISTRY ABB=ON PLU=ON (207111-98-6/BI OR
116978-12-2/BI OR 148294-93-3/BI OR 116412-30-7/BI OR
123514-78-3/BI OR 367633-06-5/BI OR 442703-09-5/BI OR
449216-82-4/BI OR 449225-92-7/BI OR 459146-74-8/BI OR
459146-76-0/BI OR 459146-77-1/BI OR 459146-78-2/BI OR
459146-82-8/BI OR 459146-86-2/BI OR 459146-88-4/BI OR
493572-11-5/BI OR 497267-31-9/BI)

L3 ANSWER 1 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN 497267-31-9 REGISTRY
CN INDEX NAME NOT YET ASSIGNED
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 138:164734

L3 ANSWER 2 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN 493572-11-5 REGISTRY
CN GenBank BAC31430 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAC31430 (Translated from: GenBank AK042994)
SQL 125
MF Unspecified
CI MAN

REFERENCE 1: 138:164520

L3 ANSWER 3 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN 459146-88-4 REGISTRY
CN L-Aspartic acid, L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl-, (1.fwdarw.1')-disulfide with L-cysteinyl-D-arginyl-D-arginyl-D-arginyl-D-arginyl-D-arginyl-D-arginyl-D-arginyl-D-argininamide (9CI) (CA INDEX NAME)
SQL 17,9,8
MF C87 H149 N41 O23 S2

REFERENCE 1: 137:237523

REFERENCE 1: 137:237523

REFERENCE 1: 137:237523

REFERENCE 1: 137:237523

REFERENCE 1: 137:237523

REFERENCE 1: 137:237523

10/007363

CN L-Lysinamide, L-cysteinyl-L-arginyl-L-glutaminyl-L-isoleucyl-L-lysyl-L-isoleucyl-L-tryptophyl-L-phenylalanyl-L-glutaminyl-L-asparaginyl-L-arginyl-L-arginyl-L-methionyl-L-lysyl-L-tryptophyl-L-lysyl-, (1.fwdarw.1')-disulfide with L-cysteinyl-L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl-L-aspartic acid (9CI) (CA INDEX NAME)
SQL 26,17,9
MF C149 H231 N47 O35 S3

REFERENCE 1: 137:237523

L3 ANSWER 10 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **449225-92-7** REGISTRY
CN 195: PN: US20020110811 SEQID: 195 unclaimed protein (9CI) (CA INDEX NAME)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 137:181594

L3 ANSWER 11 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **449216-82-4** REGISTRY
CN Kinase (phosphorylating), protein, C.epsilon. (human dominant-negative isoenzyme Nv-13) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 104: PN: US20020110811 SEQID: 104 claimed protein
SQL 156
MF Unspecified
CI MAN

REFERENCE 1: 137:181594

L3 ANSWER 12 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **442703-09-5** REGISTRY
CN 2: PN: WO02055664 SEQID: 2 unclaimed protein (9CI) (CA INDEX NAME)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 137:104169

L3 ANSWER 13 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **367633-06-5** REGISTRY
CN Protein (mouse clone P16054) (9CI) (CA INDEX NAME)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 135:327323

L3 ANSWER 14 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN **207111-98-6** REGISTRY
CN L-Aspartic acid, L-histidyl-L-.alpha.-aspartyl-L-alanyl-L-prolyl-L-isoleucylglycyl-L-tyrosyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: US20020168354 SEQID: 2 claimed
CN 1: PN: WO02078600 SEQID: 2 claimed protein

10/007363

SQL 8
MF C39 H54 N10 O14

REFERENCE 1: 137:363111

REFERENCE 2: 137:289003

REFERENCE 3: 137:237523

REFERENCE 4: 134:160633

REFERENCE 5: 132:44701

REFERENCE 6: 128:317275

L3 ANSWER 15 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN 148294-93-3 REGISTRY
CN Kinase (phosphorylating), protein (human clone E3 C isoenzyme .epsilon. reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN Protein (human clone Q02156)
CN Protein kinase C-.epsilon. (human clone E3 reduced)
SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 135:327323

REFERENCE 2: 119:23577

L3 ANSWER 16 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN 123514-78-3 REGISTRY
CN Kinase (phosphorylating), protein (mouse clone .lambda.61PKC-.epsilon. C isoenzyme .epsilon. reduced) (9CI) (CA INDEX NAME)

SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 111:227755

L3 ANSWER 17 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN 116978-12-2 REGISTRY
CN Kinase (phosphorylating), protein (rat brain clone .lambda.CKR.epsilon.41 C isoenzyme .epsilon. reduced) (9CI) (CA INDEX NAME)

SQL 737
MF Unspecified
CI MAN

REFERENCE 1: 113:53672

REFERENCE 2: 109:185985

L3 ANSWER 18 OF 18 REGISTRY COPYRIGHT 2003 ACS
RN 116412-30-7 REGISTRY
CN Kinase (phosphorylating), protein (rabbit clone RP38/R4 C protein moiety reduced) (9CI) (CA INDEX NAME)

SQL 736

10/007363

MF Unspecified
CI MAN

REFERENCE 1: 110:52097

FILE 'HOME' ENTERED AT 12:44:03 ON 14 MAR 2003